

Result No.	Score	Query	Match	Length	DB ID	Description
1	1149	100.0	288	2	A45803	B-cell-restricted antigen B7 precursor - human
2	1085	94.4	289	2	G00031	B7 protein - red-C
3	738	64.2	299	2	146690	CDB80 precursor - r
4	601.5	52.3	321	2	154766	B-lymphocyte activ
5	561	48.8	309	2	149503	B-lymphocyte activ
6	182	15.8	329	1	A48754	B7-2 antigen - hum
7	152	13.2	309	2	149522	gene B7-2 protein
8	140.5	12.2	330	2	146691	CDB6 precursor - r
9	133.5	11.6	583	2	139428	BARF1 protein - hu
10	129	11.2	221	1	Q0848	butyrophilin precursor molecule
11	127	11.1	526	2	S70587	adhesion molecule
12	122.5	10.7	588	2	JH0506	surface glycoprote
13	122.5	10.7	588	2	A45254	SPB substrate-1 pr
14	120.5	10.5	509	2	JCS288	SPB substrate-1 pr
15	120.5	10.5	513	2	JCS289	butyrophilin - mou
16	118	10.3	487	2	S65133	neural cell adhesi
17	116.5	10.1	1088	1	IJX1NL	neural cell adhesi
18	115	10.0	761	1	IJHUNG	neural cell adhesi
19	112.5	9.8	725	2	JE099	DM-GRASP precursor
20	110.5	9.6	587	2	JH0464	cell surface glyco
21	109.5	9.5	646	2	I38049	neural cell adhesi
22	109.5	9.5	853	1	IJBONC	butyrophilin - bov
23	109	9.5	526	1	A37821	protein tyrosine-P
24	109	9.5	2029	1	TDFFLK	protein tyrosine-K
25	108	9.4	871	1	I48896	protein tyrosine-K
26	108	9.4	881	1	I48667	hypothetical prote
27	107.5	9.4	5175	2	T20992	hemicentin precurs
28	107.5	9.4	5198	2	T43390	amalgam protein pr
29	106.5	9.3	333	2	A31923	

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OM protein - protein search, using sw model

Run on: April 24, 2002, 15:26:09 ; Search time 15.01 Seconds  
(without alignments)  
1096.183 Million cell updates/sec

Title: US-09-454-651B-23  
Perfect score: 1149  
Sequence: 1 GLSHFCSGVTHVTKEVKEYA.....LRVNOTENWNTIKQEHEFPDN 216

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext. 0.5

Searched: 219241 seqs, 7674552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_68:  
1: pir1:  
2: pir2:  
3: pir3:  
4: pir4:  
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	1
A45803	B-cell-restricted antigen B7 precursor - human
N;Alternate names: B-lymphocyte activation antigen B7	
C;Species : Homo sapiens (man)	
C;Date: 30-Sep-1993 #sequence-revision 30-Sep-1993 #text_change 29-Sep-1999	
C;Accession: I54495; A45803	R;Selvakumar, A.; Mohnraj, B.K.; Eddy, R.L.; Shows, T.B.; White, P.C.; Dupont, B.
Immunogenetics 36, 175-181, 1992	J. Immunol. 143, 2714-2722, 1989
A;Title: Genomic organization and chromosomal location of the human gene encoding the Ig superfamily with unique expression on activated T-cells	A;Reference number: I54495; MUID:92307753
A;Accession: I54495	A;Status: translated from GB/EMBL/DDJB
A;Molecule type: DNA	A;Cross-references: GB:M27533; PID:9184680; PIDN:AAA36045.1; PID:9306916
A;Residues: 1-288 <RSS>	A;Cross-references: GB:M27533; PID:9184680; PIDN:AAA36045.1; PID:9306916
A;Gene: GDB:CD80; CD28	A;Cross-references: GDB:21792; OMIM:112203
A;Map Position: 3q13.3-3q21	A;Map Position: 3q13.3-3q21
A;Introns: 34/1; 140/1; 234/1; 266/1	A;Introns: 34/1; 140/1; 234/1; 266/1
C;Superfamily: B-lymphocyte restricted antigen B7	C;Superfamily: B-lymphocyte restricted antigen B7
C;Keywords: transmembrane protein	C;Keywords: transmembrane protein
F;1-26/Domain: signal sequence #status predicted <SIG>	F;1-26/Domain: signal sequence #status predicted <SIG>
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Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLSHFCSGVTHVTKEVAVTSLCQHNVSVEELAQTRIYQKEKKMVLTMMMSGDMNWIPE 60	QY 1 GLSHFCSGVTHVTKEVAVTSLCQHNVSVEELAQTRIYQKEKKMVLTMMMSGDMNWIPE 60
DB 27 GLSHFCSCVTHVTKEVAVTSLCQHNVSVEELAQTRIYQKEKKMVLTMMMSGDMNWIPE 86	DB 27 GLSHFCSCVTHVTKEVAVTSLCQHNVSVEELAQTRIYQKEKKMVLTMMMSGDMNWIPE 86
QY 1 YKNRTIPDITNNLSTIVLALRPSDEGTVECVVLYERDAFKREHLAETVLSKADFTPPS 120	QY 1 YKNRTIPDITNNLSTIVLALRPSDEGTVECVVLYERDAFKREHLAETVLSKADFTPPS 120
DB 87 YKNRTIPDITNNLSTIVLALRPSDEGTVECVVLYERDAFKREHLAETVLSKADFTPPS 146	DB 87 YKNRTIPDITNNLSTIVLALRPSDEGTVECVVLYERDAFKREHLAETVLSKADFTPPS 146
QY 1 ISDFEIPPSNIRLICSTSGGFEPHLSWLNENGELAINTIVSQDPTELEIAVSSKDF 180	QY 1 ISDFEIPPSNIRLICSTSGGFEPHLSWLNENGELAINTIVSQDPTELEIAVSSKDF 180
DB 147 ISDFEIPPSNIRLICSTSGGFEPHLSWLNENGELAINTIVSQDPTELEIAVSSKDF 206	DB 147 ISDFEIPPSNIRLICSTSGGFEPHLSWLNENGELAINTIVSQDPTELEIAVSSKDF 206
QY 181 NMPTNHSMCLIKYGHLYRNQTFNWNTTKQEHFPDN 216	QY 181 NMPTNHSMCLIKYGHLYRNQTFNWNTTKQEHFPDN 216

Db	207	NMTNHSFMClikyGHLRvNQTFNWNTIKQEHPDN	242	QY	124	FEIPTSNIRRIICSTSGGPPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLFDFNMT	183
<b>RESULT 2</b>							
G00031	B7	protein - red-crowned mangabey (fragment)		Db	149	IGHEDPNVKRIRSASGGPPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLFDFNWT	208
C;Species: Cercocebus torquatus (red-crowned mangabey, white-collared mangabey)	C;Date: 11-Apr-1997 #sequence_revision 11-Apr-1997 #text_change 29-Sep-1999	C;Accession: G00031	A;Status: preliminary; translated from GB/EMBL/DBJ	QY	184	TNHISFCMLIKYGHLRVNTENWNTIKQE	211
R;Villinger, F.J.	submitted to the EMBL Data Library, January 1995	A;Accession: G00217	A;Status: preliminary; translated from GB/EMBL/DBJ	Db	209	NNESTIVCLIKYGELESQIFPWSPKPQE	236
<b>RESULT 4</b>							
I54766	B-lymphocyte activation antigen 7-1 precursor - rat	C;Species: Rattus norvegicus (Norway rat)	C;Accession: I54766	QY	124	FEIPTSNIRRIICSTSGGPPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLFDFNMT	183
A;Residues: 1-289 <VII>	A;Cross-references: EMBL:U19833; PIDN:AAA86700.1; PID:9644784	A;Accession: I54766	A;Status: preliminary; translated from GB/EMBL/DBJ	Db	149	IGHEDPNVKRIRSASGGPPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLFDFNWT	208
C;Genetics:	C;Accession: G00031	A;Status: preliminary; translated from GB/EMBL/DBJ	A;Accession: I54766	QY	184	TNHISFCMLIKYGHLRVNTENWNTIKQE	211
A;Gene: B7	C;Superfamily: B-lymphocyte restricted antigen B7	C;Accession: I54766	A;Accession: I54766	Db	209	NNESTIVCLIKYGELESQIFPWSPKPQE	236
<b>RESULT 5</b>							
LSHFCSGVIVHTVKEKEVALTSCHGHSVVEELAOTRYWKEKKVLTMSGDMNWIPEY	61	Query Match Score 1085; DB 2; Length 289; Pred. No. 1.4e-80;	Best Local Similarity 95.3%; Mismatches 4; Indels 0; Gaps 0;	QY	1	GLSHFCSGVIVHTVKEKEVALTSCHGHSVVEELAOTRYWKEKKVLTMSGDMNWIPEY	59
LSHFCSGVIVHTVKEKEVALTSCHGHSVVEELAOTRYWKEKKVLTMSGDMNWIPEY	87	Matches 205; Conservative	Score 1085; DB 2; Length 289; Pred. No. 1.4e-80;	Db	31	GLLQITSGGIVEVQVSKSREKAIALSKCYSQKHDRLVMSVTSGVPFWP	90
KRTTIDITNNLSIVTLARPSDEGYECVVLKYERDAFKREHLAEVTLSVKADPPTPSI	121	QY	Best Local Similarity 54.4%; Mismatches 35; Indels 1; Gaps 1;	QY	60	EYKNRTIDITNNLSIVTLARPSDGTGTYECVVLKYERDAFKREHLAEVTLSVKADPPTPSI	119
KRTTIDITNNLSIVTLARPSDEGYECVVLKYERDAFKREHLAEVTLSVKADPPTPSI	147	Db	Matches 112; Conservative	QY	91	KYKNRTIDYDANNYPSLQLGILSLSGDTYCVQVYVVKHATVYEVSLADDFPTP	150
SDFEITPSNIRRIICSTSGGPPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLFDFN	181	QY	Mismatches 58; Indels 1; Gaps 1;	Db	120	SISDFEILPTSMIRRICSTSGGPPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLFDFN	179
TDFEIDPSNIRRIICSTSGGPPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLFDFN	207	Db	Score 601.5; DB 2; Length 321; Pred. No. 2.2e-41;	QY	151	NITEVGNPNSADIKRITCEASGGFPKPLRSWLENGEELNAINTTVSQDPESELYTISSQLD	210
MTTNHSFMClikyGHLRvNQTFNWNTIKQEHPDN	216	QY	Best Local Similarity 54.4%; Mismatches 35; Indels 1; Gaps 1;	Db	180	FNMTINHSFmLIKYGHLRvNQTFNWNTIKQEHPDN	205
MTTNHSFVClikyGHLRvNQTFNWNTIKQEHPDN	242	Db	Score 601.5; DB 2; Length 321; Pred. No. 2.2e-41;	QY	211	FNATVDHFIDCFIEYGAHVQSQNFTW	236
<b>RESULT 3</b>							
I46690	CD80 precursor - rabbit	A;Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecule	A;Accession: I46690	QY	149503	B-lymphocyte activation antigen 7 precursor - mouse	149503
C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 29-Sep-1999	C;Species: Oryctolagus cuniculus (domestic rabbit)	A;Accession: I46690	A;Accession: I46690	Db	149503	N;Alternate names: MB7-2	149503
R;Isoono, T.; Seto, A.	A;Status: preliminary; translated from GB/EMBL/DBJ	A;Status: preliminary; translated from GB/EMBL/DBJ	A;Status: preliminary; translated from GB/EMBL/DBJ	QY	149503	C;Species: Mus musculus (house mouse)	149503
Immunogenetics 42, 217-220, 1995	A;Accession: I46690	A;Accession: I46690	A;Accession: I46690	Db	149503	C;Accession: I49503; S17291; 149521	149503
A;Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecule	A;Accession: I46690	A;Accession: I46690	A;Accession: I46690	QY	149503	R;Selvakumar, A.; White, P.C.; Dupont, B.	149503
A;Residues: 1-39 <ISO>	A;Status: preliminary; translated from GB/EMBL/DBJ	A;Status: preliminary; translated from GB/EMBL/DBJ	A;Status: preliminary; translated from GB/EMBL/DBJ	Db	149503	ImmunoGenetics 38, 292-295, 1993	149503
A;Cross-references: GB:049843; PID:9755096; PIDN:BAAB08643.1; PID:9755097	A;Accession: I46690	A;Accession: I46690	A;Accession: I46690	QY	149503	A;Title: Genomic organization of the murine B-lymphocyte activation antigen B7	149503
C;Superfamily: B-lymphocyte restricted antigen B7	A;Accession: I46690	A;Accession: I46690	A;Accession: I46690	Db	149503	A;Reference number: S17291; MUID:9330789	149503
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I46690	CD80 precursor - rabbit	A;Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecule	A;Accession: I46690	QY	64	Query Match Score 738; DB 2; Length 299; Pred. No. 1.8e-52;	64.2%
C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 29-Sep-1999	C;Species: Oryctolagus cuniculus (domestic rabbit)	A;Accession: I46690	A;Accession: I46690	Db	64	Mismatches 36; Indels 0; Gaps 0;	63.9%
R;Isoono, T.; Seto, A.	A;Status: preliminary; translated from GB/EMBL/DBJ	A;Status: preliminary; translated from GB/EMBL/DBJ	A;Status: preliminary; translated from GB/EMBL/DBJ	QY	64	Best Local Similarity 63.9%; Mismatches 36; Indels 0; Gaps 0;	63.9%
Immunogenetics 42, 217-220, 1995	A;Accession: I46690	A;Accession: I46690	A;Accession: I46690	Db	64	Score 64.2%; DB 2; Length 299; Pred. No. 1.8e-52;	64.2%
A;Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecule	A;Accession: I46690	A;Accession: I46690	A;Accession: I46690	QY	64	Matches 133; Conservative	Score 64.2%; DB 2; Length 299; Pred. No. 1.8e-52;
A;Residues: 1-39 <ISO>	A;Status: preliminary; translated from GB/EMBL/DBJ	A;Status: preliminary; translated from GB/EMBL/DBJ	A;Status: preliminary; translated from GB/EMBL/DBJ	Db	64	Mismatches 36; Indels 0; Gaps 0;	63.9%
A;Cross-references: GB:049843; PID:9755096; PIDN:BAAB08643.1; PID:9755097	A;Accession: I46690	A;Accession: I46690	A;Accession: I46690	QY	64	Score 64.2%; DB 2; Length 299; Pred. No. 1.8e-52;	64.2%
C;Superfamily: B-lymphocyte restricted antigen B7	A;Accession: I46690	A;Accession: I46690	A;Accession: I46690	Db	64	Matches 133; Conservative	Score 64.2%; DB 2; Length 299; Pred. No. 1.8e-52;
<b>RESULT 5</b>							
I46690	CD80 precursor - rabbit	A;Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecule	A;Accession: I46690	QY	4	HFSSGVIVHTVKEKEVALTSCHGHSVVEELAOTRYWKEKKVLTMSGDMNWIPEY	63
C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 29-Sep-1999	C;Species: Oryctolagus cuniculus (domestic rabbit)	A;Accession: I46690	A;Accession: I46690	Db	29	HSSGQSYTKSKYEMALSCDDNMISIDELARNRIVWQDQVNLISGQVWPEYKN	88
R;Isoono, T.; Seto, A.	A;Status: preliminary; translated from GB/EMBL/DBJ	A;Status: preliminary; translated from GB/EMBL/DBJ	A;Status: preliminary; translated from GB/EMBL/DBJ	QY	64	MTTNHSFMClikyGHLRvNQTFNWNTIKQEHPDN	123
Immunogenetics 42, 217-220, 1995	A;Accession: I46690	A;Accession: I46690	A;Accession: I46690	Db	89	RTFPDIINNLSSMLAURLSDRGTCTVQQNKNGSFREHLTSVLSIRADFVPPSTD	148
A;Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecule	A;Accession: I46690	A;Accession: I46690	A;Accession: I46690	QY	64	MTTNHSFMClikyGHLRvNQTFNWNTIKQEHPDN	123
A;Residues: 1-39 <ISO>	A;Cross-references: GB:049843; PID:9755096; PIDN:BAAB08643.1; PID:9755097	A;Accession: I46690	A;Accession: I46690	Db	89	RTFPDIINNLSSMLAURLSDRGTCTVQQNKNGSFREHLTSVLSIRADFVPPSTD	148
C;Superfamily: B-lymphocyte restricted antigen B7	A;Cross-references: GB:049843; PID:9755096; PIDN:BAAB08643.1; PID:9755097	A;Accession: I46690	A;Accession: I46690	QY	64	MTTNHSFMClikyGHLRvNQTFNWNTIKQEHPDN	123
<b>RESULT 5</b>							
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C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 29-Sep-1999	C;Species: Oryctolagus cuniculus (domestic rabbit)	A;Accession: I46690	A;Accession: I46690	Db	149503	J. Exp. Med. 174, 625-631, 1991	149503
R;Isoono, T.; Seto, A.	A;Status: preliminary; translated from GB/EMBL/DBJ	A;Status: preliminary; translated from GB/EMBL/DBJ	A;Status: preliminary; translated from GB/EMBL/DBJ	QY	149503	A;Title: Structure, expression, and T cell costimulatory activity of the murine homolog of the murine B-lymphocyte activation antigen B7	149503
Immunogenetics 42, 217-220, 1995	A;Accession: I46690	A;Accession: I46690	A;Accession: I46690	Db	149503	A;Reference number: S17291; MUID:91341422	149503
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<b>RESULT 5</b>							
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Immunogenetics 42, 217-220, 1995	A;Accession: I46690	A;Accession: I46690	A;Accession: I46690	Db	149503	A;Reference number: S17291; MUID:91341422	149503
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C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 29-Sep-1999	C;Species: Oryctolagus cuniculus (domestic rabbit)	A;Accession: I46690	A;Accession: I46690	Db	149503	ImmunoGenetics 38, 292-295, 1993	149503
R;Isoono, T.; Seto, A.	A;Status: preliminary; translated from GB/EMBL/DBJ	A;Status: preliminary; translated from GB/EMBL/DBJ	A;Status: preliminary; translated from GB/EMBL/DBJ	QY	149503	A;Title: Genomic organization of the murine B-lymphocyte activation antigen B7	149503
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<b>RESULT 5</b>							
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C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 29-Sep-1999	C;Species: Oryctolagus cuniculus (domestic rabbit)	A;Accession: I46690	A;Accession: I46690	Db	149503	ImmunoGenetics 38, 292-295, 1993	149503
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Immunogenetics 42, 217-220, 1995	A;Accession: I46690	A;Accession: I46690	A;Accession: I46690	Db	149503	A;Reference number: S17291; MUID:91341422	149503
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<b>RESULT 5</b>							
I46690	CD80 precursor - rabbit	A;Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecule	A;Accession: I46690	QY	149503	R;Selvakumar, A.; White, P.C.; Dupont, B.	149503
C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 29-Sep-1999	C;Species: Oryctolagus cuniculus (domestic rabbit)	A;Accession: I46690	A;Accession: I46690	Db	149503	ImmunoGenetics 38, 292-295, 1993	149503
R;Isoono, T.; Seto, A.	A;Status: preliminary; translated from GB/EMBL/DBJ	A;Status: preliminary; translated from GB/EMBL/DBJ	A;Status: preliminary; translated from GB/EMBL/DBJ	QY	149503	A;Title: Genomic organization of the murine B-lymphocyte activation antigen B7	149503
Immunogenetics 42, 217-220, 1995	A;Accession: I46690	A;Accession: I46690	A;Accession: I46690	Db	149503	A;Reference number: S17291; MUID:91341422	149503
A;Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecule	A;Accession: I46690	A;Accession: I46690	A;Accession: I46690	QY	149503	A;Accession: I49503; MUID:91341422	149503
A;Residues: 1-39 <ISO>	A;Cross-references: GB:049843; PID:9755096; PIDN:BAAB08643.1; PID:9755097	A;Accession: I46690	A;Accession: I46690	Db	149503	A;Accession: I49503; MUID:91341422	149503
C;Superfamily: B-lymphocyte restricted antigen B7	A;Cross-references: GB:049843; PID:9755096; PIDN:BAAB08643.1; PID:9755097	A;Accession: I46690	A;Accession: I46690	QY	149503	A;Accession: I49503; MUID:91341422	149503
<b>RESULT 5</b>							

R;Inobe, M.; Linsley, P.S.; Ledbetter, J.A.; Nagai, Y.; Tamakoshi, M.; Ueda, T.  
Biochem. Biophys. Res. Commun. 200, 443-449, 1994.

A;Title: Identification of an alternatively spliced form of the murine homologue of B7.  
A;Reference number: I49521; MUID: 94220123  
A;Accession: I49521  
A;Molecule type: mRNA  
A;Residues: 1-143 238-274, 'R', 279-309 <RE2>  
A;Cross-references: GB:DI6220; NID:950518; PIDN:BA03748.1; PID:994763  
C;Genetics:  
A;Gene: B7  
A;Introns: 37/1; 143/1; 237/1; 275/1  
C;Superfamily: B-lymphocyte restricted antigen B7  
C;Keywords: alternative splicing

Query Match 48 8%; Score 561; DB 2; Length 309;  
Best Local Similarity 50.7%; Pred. No. 3.9e-38;  
Matches 104; Conservative 41; Mismatches 58; Indels 2; Gaps 2; Result 7

Qy 12 VTKKEVATLSCGHNVSVEELAQTRIYQKEKRMVLTNNMSGDNNIWIPEYKNRTIFTIN 71  
Db 42 LISKSYKDVLLPCRYNSPHEDESEDRYHQKHDKVVLSTAGKIKWPEVKNRFLYDNT- 100

Qy 72 NLSIVILALRPSDEGTETCVVLYKEDKFREHLAEVTLSVKADEPTPSISDFELPTSNI 131  
Db 101 YSLILIGLVLSDRDTYSCVYQKERGTYEKVHIALVKLSIAFESTUPNTIESGNPSADT 160

Qy 132 RRIICSTGGFPPEPHLSWLENGEELNAINTVSQDPETELYAVSSKLDNMNTNHSFMCIL 191  
Db 161 KRITCPASGGFPKPRFESWLNGRELPGINTTISQDPESELYTISQLDNTNTRHTIKCL 220

Qy 192 IKYGLHRVNTENWTTKQEPFDN 216  
Db 221 IKYDAHVSEFTWERKPPDE-PDS 244

\* RESULT 6

A48754  
B7-2 antigen - human  
A;Alternate names: B70 glycoprotein; CD86 antigen; CTLA-4 counter-receptor  
C;Species: Homo sapiens (man)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999  
C;Accession: A48754; S39055  
B;Freeman, G.J.; Grubben, J.G.; Boussiots, V.A.; Ng, J.W.; Restivo Jr., V.A.; Lombard, Science 262, 909-911, 1993  
A;Title: Cloning of B7-2: a CTLA-4 counter-receptor that costimulates human T cell prolif  
A;Reference number: A48754; MUID: 94053735  
A;Accession: A48754  
A;Molecule type: mRNA  
A;Residues: 1-329 <RE2>  
A;Cross-references: GB:L25259; NID:9416368; PIDN:AA58389.1; PID:9416369  
A;Note: it is uncertain whether Met-1 or Met-7 is the initiator  
R;Azuma, M.; Ito, D.; Yagita, H.; Okumura, K.; Phillips, J.H.; Lanier, L.L.; Somozza, C.  
A;Title: B70 antigen is a second ligand for CTLA-4 and CD28.  
A;Reference number: S39055; MUID: 94050123  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 7-329 <AZU>  
A;Cross-references: GB:U04343; NID:9439838; PIDN:AA03814.1; PID:9439839  
C;Genetics:  
A;Gene: GDB:CD86; CD28LG2  
A;Cross-references: GDB:433597; OMIM: 601020  
A;Map position: 3q13.3-3q21  
C;Superfamily: B7-2 antigen  
C;Keywords: glycoprotein

Query Match 15.8%; Score 182; DB 1; Length 329;  
Best Local Similarity 29.0%; Pred. No. 2e-07;

Matches 60; Conservative 38; MisMatches 71; Indels 38; Gaps 10;  
Qy 18 EVATLSC ---GHNVSVEELAQTRIYQKEKRMVLTNNMSGDNNIWIPEYKNRTIFTDI 69  
Db 34 ETADLPCOFANSONQNSLSELV --VFWQDENYLNEVYLGEKEFDVSQKMYRTSFD- 89

Qy 70 TNNSIVILALRPSDEGTETCVVLYKEDKFREHLAEVTLSVKADEPTPSISDFELPTS 129  
Db 90 SDSWTLRLHNLQIKDQKGYQCTIHHKKPTGMIRLHMNSLVLANFSEPEI ---VPI5 145

Qy 130 NIR ---RRIICSTGGFPPEPHLSWLENGEELNAINTVSQDPETELYAVSSKLDNMNTNHSFMCIL 175  
Db 146 NITENVYINLTCSSTHGYPPEPKKMSVL ---LRTKNSTIEYDGIMQKSODDNVTELYDVS 200

Qy 176 SKLDF ---NMNTNHSFMCMLIKYGHLRV 199  
Db 201 ISLSVSPDPDVTSNMNTIFCILETDKTRL 227

RESULT 7

I49522  
gene B7-2 protein - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jul-1996 #text\_change 23-Jul-1999  
C;Accession: I49522  
R;Freeman, G.J.; Borriello, F.; Hodes, R.J.; Reiser, H.; Gribben, J.G.; Ng, J.W.; Kim J. Exp. Med. 178, 2185-2192, 1993  
A;Title: Murine B7-2, an alternative CTLA4 counter-receptor that costimulates T cell A;Reference number: I49522; MUID: 9405585  
A;Accession: I49522  
A;Status: preliminary, translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Cross-references: GB:L25606; NID:9432478; PIDN:AAA79770.1; PID:9432479  
C;Genetics:  
A;Gene: B7-2  
C;Superfamily: B7-2 antigen

Query Match 13.2%; Score 152; DB 2; Length 309;  
Best Local Similarity 16.1%; Pred. No. 4.9e-05;  
Matches 52; Conservative 43; MisMatches 78; Indels 26; Gaps 10;

Qy 20 ATLSC ---GHNVSVEELAQTRIYQKEKRMVLTNNMSGDNNIWIPEYKNRTIFTDI 69  
Db 36 AYLPCCPTKAQNISLSELV --VFWQOQKLVLYEHYLGTEILDSVA ---AKYLGRIISFD- 89

Qy 70 TNNSIVILALRPSDEGTETCVVLYKEDKFREHLAEVTLSVKADEPTPSISDFELPTS 127  
Db 90 RNNWTLRLHNLQIKDQKGYQCTIHHKKPTGMIRLHMNSLVLANFSEPEIQLAQNV 147

Qy 128 TSNR-FRIICSTGGFPPEPHLSW ---LNGEELNAINTVSQDPETELYAVSSKLDNMNTNHSFMCIL 182  
Db 148 TGNSGINLTCSTSQGHKPCKAMFLITINSTNEYGDNMNOISQDNTELFISNSLSSLSPD 207

Qy 183 -TNHSPCMCLIKYGHLRV 200  
Db 208 GYWHMTVVCVLETESMMKIS 226

RESULT 8

I46691  
CD86 precursor - rabbit  
C;Species: Oryctolagus cuniculus (domestic rabbit)  
C;Date: 14-Feb-1997 #sequence\_revision 14-Feb-1997  
C;Accession: I46691  
R;Isono, T.; Seto, A.  
Immunogenetics 42, 217-220, 1995  
A;Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory mole A;Reference number: I46691  
A;Accession: I46691  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA

A;Residues: 1-330 <ISO>  
A;Cross-references: GB:D49842; NID:9755098; PIDN:BAA08642.1; PID:9755099  
C;Superfamily: B7-2 antigen

Query Match 12.28; Score 140.5; DB 2; Length 330;  
Best Local Similarity 27.48%; Pred. No. 0.00045; Indels 41; Gaps 12;  
Matches 60; Conservative 34; Mismatches 84; C;Superfamily: human herpesvirus 4 BARF1 protein

Qy 18 EVATLSCGHNVSVEELAQTRIYWKREKKMVTMM----SGDMNINPEKVKRRTIEDITN- 71  
Db 34 KADLPQFQTNQSRSUJELVFWQDDERLYELFLGREKPDNVPKYIGRTSFQESW 93  
Qy 72 NISIVTILALRPSDEGTYECVVLKYERDAFKREHHLAETVLSKVADPPTPSISDFEPITSNI 131  
Db 94 NQLHNWQIK--DKGYQQCFYHHRGAKGLYTIQYOMNSELSVLANFTQPELT---LISNI 147  
Qy 132 RR-----LICSTGGGPPEPHSLWLENGEELNAINTV-----SDPETELY-AVSS 176  
Db 148 TRANSATNATCSCSVQG1PEPKMKF---VLKTENATTEDGVTEKSQDNVTGLYNISIG 203  
Qy 177 KLDFF-NKTTNISLTCQHNTKQHFF 214  
Db 204 SITEFDDIRNATIYCVL-----QTESTETYSQ-HFP 233

RESULT 9

I39428

alcam - human

C;Species: Homo sapiens (man)

C;Accession: Sep-1996 #sequence\_revision 06-Sep-1996 #text\_change 21-Jul-2000

- R;Bowen, M.A.; Patel, D.D.; Li, X.; Modrell, B.; Malacko, A.R.; Wang, W.C.; Marquardt, F.J.; Exp. Med. 181, 2213-2220, 1995  
A;Title: Cloning, mapping, and characterization of activated leukocyte-cell adhesion mol  
A;Reference number: I39428; MUID:95279947  
A;Accession: I39428  
A;Status: preliminary; translated from GB/EMBL/DDJB  
A;Molecule type: mRNA  
A;Residues: 1-583 <PES>  
A;Cross-references: GB:L38608; NID:9886257; PIDN:AAB59499.1; PID:9886258

Query Match 11.6%; Score 133.5; DB 2; Length 583;  
Best Local Similarity 24.5%; Pred. No. 0.0034; Indels 35; Gaps 7;  
Matches 37; Conservative 35; Mismatches 54; C;Species: human herpesvirus 4 (strain B95-8)

Qy 59 PEYKARTIFDNNLPSDEGTYECVVLKYERDAFKREHHLAETVLSVKADFPT 118  
Db 84 PEYKDR--LNLSENTYLISNARISDEKFVCMLYT-EDWFEAFTIVK-----FQK 133  
Qy 119 PSISDFE-----IPTSNIRRI-LGSTGGFPPEPHSLWLENGEELNAINTV-----SQD 166  
Db 134 PSKPEIVSKAFLFETEQLKLIGDCEISDYPDGNTWYRNGKVLHPLEGAVVTFKKEND 193  
Qy 167 PETELYAYSSKLDEFMT---TNHSFMCILKY 194  
Db 194 PVTQLYTMSTLEYKTKADIQMFETCSVY 224

RESULT 10  
QBE88

BARF1 protein - human herpesvirus 4

Epstein-Barr virus

C;Date: 25-Feb-1985 #sequence\_revision 25-Feb-1985 #text\_change 16-Jul-1999  
C;Accession: B43045; A0379; S33058  
R;Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrell, B.G.  
Mol. Biol. Med. 1, 21-45, 1983  
A;Title: Sequence analysis of the 17,166 bp ECOLI fragment C of B95-8 Epstein-Barr virus  
A;Reference number: A93065; MUID:85035713  
A;Molecule type: DNA  
A;Residues: 1-221 <BAN>

RESULT 11  
JH0506

adhesion molecule SC1 precursor - chicken

C;Species: Gallus gallus (chicken)  
C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 21-Jul-2000  
C;Accession: JH0506; PS2270  
R;Tanaka, H.; Matsui, T.; Agata, A.; Tomura, M.; Kubota, I.; McFarland, K.C.; Kohr, B.  
Neuron 7, 535-545, 1991  
A;Title: Molecular cloning and expression of a novel adhesion molecule, SC1.

A; Reference number: JH0506; MUID:92030150  
 A; Molecule type: mRNA  
 A; Residues 1-58 <YAN>  
 A; Cross-references: GB:S63276; NID:9238000; PIDN:AAB20170.1; PID:9238001  
 A; Experimental source: embryo  
 A; Accession: PS270  
 A; Molecular type: protein  
 A; Residues: 34-48 <TAAN1>  
 C; Comment: This protein is uniquely and transiently expressed on spinal cord motoneurons  
 C; Keywords: glycoprotein, transmembrane protein  
 F; 1-33/Domain: signal sequence #status predicted <SIG>  
 F; 34-588/Product: adhesion molecule SC1 #status predicted <ADH>  
 F; 500-523/Domain: transmembrane #status predicted <TRA>  
 F; 101,173,199,271,312,366,462,485,504/Binding site: carbohydrate (Asn) (covalent) #status  
 A; Gene: shps-1  
 A; Map position: 2

Query Match 10.7%; Score 122.5; DB 2; Length 588;  
 Best Local Similarity 25.7%; Pred. No. 0.027; Indels 27; Gaps 8;  
 Matches 39; Conservative 32; Mismatches 54; Indels 27; Gaps 8;

Qy 59 PEYKNRTIFDTNNLISIVILALRSPDEGTETCVVLYKERYDAFKRHLAEVTLYSKADFPT 118  
 Db 90 EDYKDR -LSSENNTLISKARISDEKRFVCLMVT-EDDVSEEPITVVKV-----FKQ 139  
 Qy 119 PS-----ISDFEIPTSNIRI -ICSTGGFPPEHLSWLENG-----EELNAINTTVSQ 165  
 Db 140 PSQPELHQAF -LETEKLKMLGECVRDSLQPEGVNTWIKGRVLQPVEEVVNLRKVE 198  
 Qy 166 DPETELYAVSSKLDNFMT --TNHSPMCLIKY 194  
 Db 199 NRSTGLFTMSSLQMPTEKDANAKETCIVY 230

RESULT 13  
 A45254 surface glycoprotein BEN precursor - chicken  
 C; Date: 27-Jun-1994 #sequence\_revision 27-Jun-1994 #text\_change 21-Jul-2000  
 C; Accession: A45254; S19202  
 F; Pourquier, O.; Corbel, C.; Le Caer, J.P.; Rossier, J.; Le Douarin, N.M.  
 Proc. Natl. Acad. Sci., U.S.A. 89, 5261-5265, 1992  
 A; Title: BEN, a surface glycoprotein of the immunoglobulin superfamily, is expressed in  
 A; Reference number: A45254; MUID:92302244  
 A; Accession: A45254  
 A; Status: preliminary  
 A; Molecule type: mRNA  
 A; Residues 1-58 <POU>  
 A; Cross-references: EMBL:X64301; NID:963087; PIDN:CAA45579.1; PID:963088  
 C; Keywords: glycoprotein

Query Match 10.7%; Score 122.5; DB 2; Length 588;  
 Best Local Similarity 25.7%; Pred. No. 0.027; Indels 27; Gaps 8;  
 Matches 39; Conservative 32; Mismatches 54; Indels 27; Gaps 8;

Qy 59 PEYKNRTIFDTNNLISIVILALRSPDEGTETCVVLYKERYDAFKRHLAEVTLYSKADFPT 118  
 Db 90 EDYKDR -LSSENNTLISKARISDEKRFVCLMVT-EDDVSEEPITVVKV-----FKQ 139  
 Qy 119 PS-----ISDFEIPTSNIRI -ICSTGGFPPEHLSWLENG-----EELNAINTTVSQ 165  
 Db 140 PSQPELHQAF -LETEKLKMLGECVRDSLQPEGVNTWIKGRVLQPVEEVVNLRKVE 198  
 Qy 166 DPETELYAVSSKLDNFMT --TNHSPMCLIKY 194  
 Db 199 NRSTGLFTMSSLQMPTEKDANAKETCIVY 230

RESULT 14  
 JG5288 substrate-1 protein, 509 - mouse  
 C; Species: Mus musculus (house mouse)

C; Date: 16-Apr-1997 #sequence\_revision 09-May-1997 #text\_change 20-Jun-2000  
 C; Accession: JC5288  
 A; Molecule type: mRNA  
 A; Residues: 1-509 <YAM>  
 A; Cross-references: DDBJ:D87967; NID:91864012; PIDN:BAA13520.1; PID:91864013  
 C; Comment: This protein is a glycosylated receptor-like protein and plays a role in c acts as a docking protein and induce translocation of Shp-2 from the cytosol to the C; Genetics:  
 A; Gene: shps-1  
 A; Map position: 2

Query Match 10.5%; Score 120.5; DB 2; Length 509;  
 Best Local Similarity 25.9%; Pred. No. 0.032; Indels 39; Gaps 15;  
 Matches 59; Conservative 42; Mismatches 88; Indels 39; Gaps 15;

Qy 3 SHFCGVY----IHTVKEVYEA-----TLSCGHNVNSVEELAQTRIYWK---EKMV 48  
 Db 23 SCFCGTGVTGKELKVQDEKSYSVAAGDSTVLNC--TLLTSLPVGPPIKWRGVGQSRLLI 79

Qy 49 TMMMSGDNNIWPYKRNRTIFDT--NNU--SIVILALRSPDSEGYECVLYKYEKDAFKREH 104  
 Db 80 YSFTEGH -FPRVTN -VSDATKRNNNDFSRISNTVPEDAGTYCYC -KFOKGPSSEPD 133

Qy 105 L-----AEVPLSVKADEPPTS -ISDFEIPTSNIRIICSTGGFPPEHLSWLENGEL 156  
 Db 134 EIQQGGTEVYVLAQSPPEVGPADRGIPDQKV -NETCKSHGFESPNTIJKWFQOEL 192

Qy 157 NAINTVSDPDTELYAVS --KLDPMTNHSMEMCLIKYHLRVNQT 202  
 Db 193 HHLETIVNPSGKVNNSISSTYRVVLSMDVHS -KVICEVAHTLDRS 239

RESULT 15  
 JC5289 SHP substrate-1 protein, 513 - mouse  
 C; Species: Mus musculus (house mouse)  
 C; Date: 16-Apr-1997 #sequence\_revision 09-May-1997 #text\_change 20-Jun-2000  
 C; Accession: JC5289  
 A; Yamao, T.; Matczak, T.; Amano, K.; Matsuda, Y.; Takahashi, N.; Ochi, F.; Fujioka, B.; Biochem. Biophys. Res. Commun. 231, 61-67, 1997  
 A; Title: Mouse and human Shp-2: Molecular cloning of cDNAs and chromosomal localization  
 A; Reference number: JC5287; MUID:97223399  
 A; Contents: Brain  
 A; Accession: JC5289  
 A; Molecule type: mRNA  
 A; Residues: 1-513 <YAM>  
 A; Cross-references: DDBJ:D87968; NID:91864014; PIDN:BAA13521.1; PID:91864015  
 C; Comment: This protein is a glycosylated receptor-like protein and plays a role in c acts as a docking protein and induce translocation of Shp-2 from the cytosol to the C; Genetics:  
 A; Gene: shps-1  
 A; Map position: 2

Query Match 10.5%; Score 120.5; DB 2; Length 513;  
 Best Local Similarity 25.9%; Pred. No. 0.033; Indels 39; Gaps 15;  
 Matches 59; Conservative 42; Mismatches 88; Indels 39; Gaps 15;

Qy 3 SHFCGVY----IHTVKEVYEA-----TLSCGHNVNSVEELAQTRIYWK---EKMV 48  
 Db 23 SCFCGTGVTGKELKVQDEKSYSVAAGDSTVLNC--TLLTSLPVGPPIKWRGVGQSRLLI 79

Qy 49 TMMMSGDNNIWPYKRNRTIFDT--NNU--SIVILALRSPDSEGYECVLYKYEKDAFKREH 104  
 Db 80 YSFTEGH -FPRVTN -VSDATKRNNNDFSRISNTVPEDAGTYCYC -KFOKGPSSEPD 133

Qy 105 L-----AEVTLVKADFPPTPS-ISDFEIPTSNIIRIICSTGGFPEP-HLSWLENGEEL 156  
| | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : |  
Db 134 EIQQGGTEVYTLAKPSPEVSGPADRGIPDOKV-NFTCKSISGFSPRNTLKWFKDGEL 192  
Qy 157 NAINTTYSQDPETELYAVSS--KLDFNMNTTNHISFMCLIKYGHLRVNQT 202  
| : | || : | | : | | : | | : | | : | | : | | : | | : | | : | | : |  
Db 193 HLELTTVNPSGKNSVSYNISSTRVVLNSMDVHS-KVICEVAHTLDRS 239

Search completed: April 24, 2002, 15:31:02  
Job time: 293 sec

SUMMARIES							
Result No.	Score	Query	Match Length	DB ID	Description		
1	114.9	100.0	288	1 CD80_HUMAN	P33681 homo sapien		
2	738	64.2	299	1 CD80_RA6T	P42070 oryctolagus		
3	561	48.8	306	1 CD80_MOUSE	Q00609 mus musculus		
4	182	15.8	329	1 CD86_HUMAN	P42081 homo sapien		
5	161	14.0	302	1 ICOL_HUMAN	Q75144 homo sapien		
6	152	13.2	309	1 CD86_MOUSE	P42082 mus musculus		
7	150.5	13.1	322	1 ICOL_MOUSE	Q9Jhj8 mus musculus		
8	140.5	12.2	330	1 CD86_RA6T	P42071 oryctolagus		
9	134.5	11.7	583	1 C166_MOUSE	Q61490 mus musculus		
10	133.5	11.6	583	1 C166_HUMAN	Q137490 homo sapien		
11	129	11.1	221	1 BRFL_EBV	P03228 epstein-bar		
12	127	11.1	526	1 BUTY_HUMAN	P03410 homo sapien		
13	122.5	10.7	598	1 C166_CHICK	P42292 gallus gallus		
14	119	10.4	524	1 BUTY_MOUSE	Q62556 mus musculus		
15	116.5	10.1	1088	1 NCAL_XENIA	P16170 xenopus laevis		
16	115	10.0	761	1 NCAL_HUMAN	P13592 homo sapien		
17	115	10.0	848	1 NCAL_HUMAN	P13591 homo sapien		
18	110.5	9.6	321	1 TCB_FLV	P11364 feline leuk		
19	109.5	9.5	646	1 MUB_HUMAN	P43121 homo sapien		
20	109.5	9.5	853	1 NCAL_BOVIN	P31836 bos taurus		
21	109	9.5	526	1 BUTY_BOVIN	P18892 bos taurus		
22	109	9.5	2029	1 LAR_DRONE	P46621 drosophila		
23	108.5	9.4	365	1 CXAR_MOUSE	P97792 mus musculus		
24	106.5	9.3	333	1 AMAL_DRONE	P15364 drosophila		
25	106.5	9.3	858	1 NCAL_RAT	P13596 rattus norvegicus		
26	105	9.1	319	1 A33_HUMAN	Q99795 homo sapien		
27	105	9.1	1091	1 NCAL_CHICK	P36335 xenopus laevis		
28	104	9.1	1092	1 NCAL_XENIA	P13594 mus musculus		
29	103.5	9.0	725	1 NCAL_MOUSE	P13595 mus musculus		
30	103	9.0	1115	1 NCAL_HUMAN	P57087 homo sapien		
31	103	9.0	298	1 VEJA_HUMAN	Q99610 gallus gallus		
32	102	8.9	1443	1 NEOL_CHICK	P62151 mus musculus		
33	101.5	8.8	403	1 RAGE_MOUSE			

ALIGNMENTS							
RESULT 1							
ID	CD80_HUMAN		STANDARD;		PRT;	288 AA.	
AC	P33681;						
DT	01-FEB-1994 (Rel. 28, Created)						
DT	01-FEB-1994 (Rel. 28, Last sequence update)						
DT	20-AUG-2001 (Rel. 40, Last annotation update)						
DE	T LYMPHOCTYE ACTIVATION ANTIGEN CD80 PRECURSOR (ACTIVATION B7-1 DE ANTIGEN) (CTLA-4 COUNTER-RECEPTOR B7-1) (BB1).						
GN	CD80 OR CD28LG1 OR CD28LG OR LA87.						
OS	Homo sapiens (Human).						
OC	Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Bivalvia; Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.						
OX	NCBI_TAXID:9606;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RC	TISSUE-Lymphoid;						
RX	MedlineID=90010147; PubMed=2794510;						
RA	Freeman G.J., Freedman A.S., Segil J.M., Lee G., Whitman J.F., Nadler L.M., Nadler B.K., Mohanraj B.K., Eddy R.L., Shows T.B., White P.C., Dupont B.; "B7, a new member of the Ig superfamily with unique expression on activated and neoplastic B cells.";						
RT	RL J Immunol. 143:2714-2722(1989); [2]						
RT	SEQUENCE FROM N.A.						
RX	MedlineID=92307753; PubMed=1377173;						
RA	Selvakumar A., Mohanraj B.K., Eddy R.L., Shows T.B., White P.C., Dupont B.; "Genomic organization and chromosomal location of the human gene encoding the B-lymphocyte activation antigen B7.";						
RT	Immunogenetics 36:175-181(1992). [3]						
RN	SEQUENCE OF 35-38.						
RX	MedlineID=91341422; PubMed=1714935;						
RA	Freeman G.J., Gray G.D., Gimmi C.D., Lombard D.B., Zhou L.-J., White M., Fingerot J.D., Gibben J.G., Nadler L.M., "Structure, expression, and T cell costimulatory activity of the murine homologue of the human B lymphocyte activation antigen B7.";						
RT	J Immunol. 154:97-105(1995). [4]						
RT	CHARACTERIZATION.						
RX	MedlineID=95038403; PubMed=7527824;						
RA	Lanier L.L., O'Fallon S., Somoza C., Phillips J.H., Linsley P.S., Okumura K., Ito D., Azuma M.; "CD80 (B7) and CD86 (B70) provide similar costimulatory signals for T cell proliferation, cytokine production, and generation of CTLs.";						
RT	J Immunol. 154:154-159(1995). [5]						
CC	- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T LYMPHOCYTE ACTIVATION. T CELL PROLIFERATION AND CYTOKINE PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS RECEPTOR.						
CC	- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.						
CC	- TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS, MACROPHAGES AND DENDRITIC CELLS.						
CC	- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS ONE C2-LIKE AND ONE V-LIKE DOMAINS.						

-!- DATABASE: NAME=PROW; NOTE=CD guide CD80 entry;  
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd80.htm".

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CC EMBL; M27533; AAA36045; 1; -.  
 DR EMBL; M63077; AAA8390; 1; -.  
 DR EMBL; M63072; AAA8390; 1; JOINED.  
 EMBL; M63073; AAA8390; 1; JOINED.  
 DR PIR; A45803; A45803; -.  
 DR MIM; 112203; -.  
 DR InterPro; IPR003599; 19.  
 DR InterPro; IPR003006; 19\_MHC.  
 DR InterPro; IPR003600; Ig-like.  
 DR SMART; SM00409; Ig; 1.  
 DR SMART; SM00410; Ig-like; 1.  
 KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;

Receptor.

FT SIGNAL	1	34	T LYMPHOCYTE ACTIVATION ANTIGEN CD80.
FT CHAIN	35	288	EXTRACELLULAR (POTENTIAL).
FT DOMAIN	35	242	POTENTIAL.
FT TRANSMEM	243	263	CYTOSOLIC (POTENTIAL).
FT DOMAIN	264	288	IG-LIKE V-TYPE DOMAIN.
FT DOMAIN	43	123	IG-LIKE C2-TYPE DOMAIN.
FT DISULFID	155	223	POTENTIAL.
FT DISULFID	50	116	POTENTIAL.
FT DISULFID	162	216	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	53	53	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	89	89	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	98	98	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	186	186	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	207	207	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	211	211	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	226	226	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	232	232	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE	288 AA;	33048 MW;	BEST LOCAL SIMILARITY 100.0%; PRED. NO. 3.6e-89; LENGTH 288; MATCHES 216; CONSERVATIVE 0; MISMATCHES -0; GAPS 0;

Qy 1 GLSHFCGSVIIHVKVEATLSCGHNVSYBELACTRIWKEKKMVLTMMSGDMNIWPE 60  
 Db 27 GLSHFCGSVIIHVKVEATLSCGHNVSYBELACTRIWKEKKMVLTMMSGDMNIWPE 86  
 Qy 61 YKNRTLFDTNNLSTVTLALRPSDEGTETYCVLYKEKDAFKREHLAETVLSKADFPPTS 120  
 Db 87 YKNRTLFDTNNLSTVTLALRPSDEGTETYCVLYKEKDAFKREHLAETVLSKADFPPTS 146  
 Sq Y 121 ISDFEPTSNIRRICSTSGFPPEPHLSWLENGEELNAINTVSQDPETELYAVSSKLDF 180  
 Db 147 ISDFEPTSNIRRICSTSGFPPEPHLSWLENGEELNAINTVSQDPETELYAVSSKLDF 206  
 Qy 181 NMTTNHSFMCMLKYGHLYRNKFNWNTTKQEHFDN 216  
 Db 207 NMTTNHSFMCMLKYGHLYRNKFNWNTTKQEHFDN 242

Query Match Score 738; DB 1; Length 299;  
 Best Local Similarity 63.9%; Pred. No. 8.9e-55; Mismatches 36; Indels 0; Gaps 0;

Qy 4 HFCSGYVTHVKVEATLSCGHNVSYBELACTRIWKEKKMVLTMMSGDMNIWPEYKN 63  
 Db 29 HFSSGJSQVTKSVKENAALSDYNSIDEALARMLYQWDQMVLSIISGOVEVPEYKN 88

Qy 64 RTIIFDTNNLSTVTLALRPSDEGTETYCVLYKEKDAFKREHLAETVLSKADFPPTS 123  
 Db 89 RTFPDINNLSLMIALRLSPKGTYTCVVKRNENGSRREHLSYSTLSRADFPVPSITD 148

Qy 124 FEIPTSNIRRICSTSGFPPEPHLSWLENGEELNAINTVSQDPETELYAVSSKLDFNMT 183

RESULT 3

CD80\_MOUSE ID CD80\_MOUSE STANDARD; PRT; 306 AA.

AC Q00609; QY 184 TNNSFMCILKYLRLRNOTNWNTTQE 211  
NNHISIVCLIKYGELSVSQTFPNSPKQOE 236

DR 209 T L Y M P H O C Y T E A C T I V A T I O N A N T I G E N C D 8 0 .

DR Transmembrane; Glycoprotein; Signal; Transmembrane;

DR Immuno-globulin domain; T-cell; Glycoprotein; Signal; Transmembrane;

KW Receptor.

FT SIGNAL 1 37

FT CHAIN 38 246 T L Y M P H O C Y T E A C T I V A T I O N A N T I G E N C D 8 0 .

FT DOMAIN 38 246 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 247 268 POTENTIAL.

FT DOMAIN 269 306 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 47 126 IG-LIKE V-TYPE DOMAIN.

FT DOMAIN 158 226 IG-LIKE V-TYPE DOMAIN.

FT DISULFID 227 246 IG-HANGE LIKE (POTENTIAL).

FT DISULFID 54 119 POTENTIAL.

FT CARBOHYD 165 219 POTENTIAL.

FT CARBOHYD 93 93 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 99 99 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 210 210 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 214 214 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 306 AA; 34589 MW; 10RADE931B8AC62 CRC64;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=B-cell;

RX MEDLINE=9134422; PubMed=1714935;

RA Gray G.S., Freeman G.J., Gianni C.D., Lombard D.B., Zhou L.J., White M., Fingerot J.D., Gibben J.G., Nadler L.M.; "Structure, expression, and T cell costimulatory activity of the murine homologue of the human B lymphocyte activation antigen B7.".

RL J. Exp. Med. 174:625-631(1991).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=B-cell;

RX MEDLINE=93307789; PubMed=7686531;

RA Selvakumar A., White P.C., Dupont B.; "Genomic organization of the mouse B-lymphocyte activation antigen B7.".

RT RT Immunogenetics 38:292-295 (1993).

CC -1- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T LYMPHOCYTES ACTIVATION T CELL PROLIFERATION AND CYTOKINE PRODUCTION IS INDUCED BY THE BINDING OF CD88 OR CTLA-4 TO THIS RECEPTOR.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS, GAMMA INTERFERON STIMULATED MONOCYTES AND NONCIRCULATING B-CELL MALIGNANCIES.

CC -1- DEVELOPMENTAL STAGE: EXPRESSED BETWEEN 4 AND 12 HOURS POST-ACTIVATION. PROTEIN WAS DETECTED AT CELL SURFACE AT 24 HOURS AND IT'S EXPRESSION WAS MAXIMAL FROM 48 TO 72 HOURS POST ACTIVATION.

CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS ONE C2-LIKE AND ONE V-LIKE DOMAINS.

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CC EMBL; X60958; CAA43291.1; DR MGD; MGI:101775; Cd80.

EMBL; L12589; AA37240.1; ALT\_SEO. DR InterPro; IPR03559; Ig.

EMBL; L12585; AA37240.1; JOINED. DR InterPro; IPR03306; Ig\_MHC.

EMBL; L12586; AA37240.1; JOINED. DR InterPro; IPR03360; Ig\_like.

EMBL; L12587; AA37240.1; JOINED. DR PIR; S17291; S17291.

EMBL; L12588; AA37240.1; JOINED.

DR MGI:101775; Cd80.

DR InterPro; IPR03559; Ig.

DR InterPro; IPR03306; Ig\_MHC.

DR InterPro; IPR03360; Ig\_like.

DR Pfam; PF00047; Ig; 2.

[3]	RN SEQUENCE OF 7-329 FROM N.A. RP RC TISSUE-Foreskin; RX MEDLINE=953311831; PubMed=7441777;	FT CARBOHYD 146 N-LINKED (GLCNAC. . .) (POTENTIAL); FT CARBOHYD 154 N-LINKED (GLCNAC. . .) (POTENTIAL); FT CARBOHYD 177 N-LINKED (GLCNAC. . .) (POTENTIAL); FT CARBOHYD 192 N-LINKED (GLCNAC. . .) (POTENTIAL); FT CARBOHYD 213 N-LINKED (GLCNAC. . .) (POTENTIAL); FT CONFLICT 27 K -> E (IN REF. 3.) SQ SEQUENCE 329 AA; 37696 MW; 65D4F3826889CFC7D CRC64;
[4]	RN CHARACTERIZATION RX MEDLINE=95088403; PubMed=7527824;	Query Match 15.8%; Score 182; DB 1; Length 329; Best Local Similarity 29.0%; Pred. No. 3.2e-08; Matches 60; Conservative 38; Mismatches 71; Indels 38; Gaps 10;
RA Lanier L.L., O'Fallon S., Somoza C., Phillips J.H., Linsley P.S.,	QY 18 EVATLSC---GHNVSVEELAQTRIYWQKEKKVMTMM---SGDMNIWPEYKNRT.FDI 69 34 ETADLPCQFANSQNSQSLSELV--VFWQDQNLVLNEVYLKEKEFKSVHSKYMGRSFSD- 89	
RA RA Green N.R., Gray G.S.; "Genomic organization of the gene coding for the costimulatory human	Db 70 TNNLSTVILALRPSDEGTTECVLVYKDAFKREHIAEVTLVKADPPTPSISDFE.LPT5 129 90 SDSWTLRHLNQLQDKGLYQCLIIHHKPTGMIRIHOMNSELVSVLANSQPEI---VPIS 145	
RL RT B-lymphocyte antigen 87-2 (CD86)."; RL Immunogenetics 42:85-89(1995).		
RN [4]	RN Engel P., Gruben J.G., Freeman G.J., Zhou L.T., Nozawa Y., Abe M., Nadler L.M., Watasa H., Tedder T.F.; "The B7-2 (B70) costimulatory molecule expressed by monocytes and activated B lymphocytes is the CD86 differentiation antigen."; Blood 84:1402-1407(1994).	QY 130 NIR---RITCSTSGCFPEPHLSWLENGELNAITV-----SQDPETELAVS 175 Db 146 NITENVYINJCSSIHGYPEPKMSVL---LRTKNTSTIEVDGIMOKSQDNVNTELDVS 200
CC CC IDENTIFICATION AS CD86.	QY 176 SKLDF--NMNTTNHFSMCLIKYGHLY 199 Db 201 ISLSVSPFDVTISNMTCFILETDKTRL 227	
CC CC BINDING CD28 OR CTLA-4 MAY PLAY A CRITICAL ROLE IN THE EARLY EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS, SUCH AS DECIDING BETWEEN IMMUNITY AND ANERGY THAT IS MADE BY T CELLS WITHIN 24 HOURS AFTER ACTIVATION.	RESULT 5 ICOL_HUMAN ID ICOL_HUMAN STANDARD; AC 07114; Q9HQD18; DT 15-JUL-1999 (Rel. 38, Created) DT 20-AUG-2001 (Rel. 40, Last sequence update) DT 20-AUG-2001 (Rel. 40, Last annotation update) DE ICOS LIGAND PRECURSOR (B7 HOMOLOG 2) (B7-H2) (B7-LIKE PROTEIN GL50) DE (B7-RELATED PROTEIN 1) (B7RP-1). GN ICOSL OR B7H2 OR B7RP1 OR KIAA0653. OS Homo sapiens (Human). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxId=9606; RN [1] RN SEQUENCE FROM N.A. (ISOFORM 1). RC TISSUE=Dendritic cell; RN PubMed=112023515; RX Wang S., Zhu G., Chapoval A.I., Dong H., Tamada K., Ni J., Chen L.; RT "Costimulation of T cells by B7-H2, a B7-like molecule that binds ICOS"; RT Blood 96:2808-2813 (2000). RN [2] RX SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION. RC TISSUE=Peripheral blood lymphocytes; RN PubMed=110007762; RX Yoshihaga S.K., Zhang M., Pistillo J., Horan T., Khare S.D., Miner K., Sonnenberg M., Boone T., Brankow D., Dai T., Delaney J., Han H., Hui A., Kohno T., Manoukian R., Whoriskey J.S., Coccia M.A.; RT "Characterization of a new human B7-related protein: B7RP-1 is the ligand to the co-stimulatory protein ICOS"; RT Int. Immunol. 12:1439-1447 (2000). RN [3] RN SEQUENCE FROM N.A. (ISOFORM 2). RC TISSUE=Leukocyte; RN PubMed=10657606; RX Ling V., Wu P.W., Farmer H.F., Bean K.M., Spaulding V., Fouser L.A., RA Leonard J.P., Hunter S.E., Zoller R., Thomas J.L., Miyashiro J.S., RA Jacobs K.A., Collins M.; RT "Identification of GL50, a novel B7-like protein that functionally binds to ICOS receptor"; RT J. Immunol. 164:1653-1657 (2000). RN [4]	
CC CC -1- TISSUE SPECIFICITY: EXPRESSED BY ACTIVATED B LYMPHOCYTES AND MONOCYTES.		
CC CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS ONE C2-LIKE AND ONE V-LIKE DOMAINS.		
CC CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD86 entry; WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd86.htm".		
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See http://www.isb-sib.ch/announce/ or send an email to licenses@isb-sib.ch).		
CC DR EMBL; 125259; AAAB58389; 1; -		
DR DR EMBL; 00434; AAAB3814; 1; -		
DR DR EMBL; 017722; AAAB86473; 1; JOINED.		
DR DR EMBL; 017717; AAAB86473; 1; JOINED.		
DR DR EMBL; 017718; AAAB86473; 1; JOINED.		
DR DR EMBL; 017719; AAAB86473; 1; JOINED.		
DR DR EMBL; 017721; AAAB86473; 1; JOINED.		
DR DR EMBL; 601020; -		
DR DR InterPro; IPR003006; Ig_MHC.		
DR DR PROSITE; PS00290; Ig_MHC; FALSE NEG.		
KW KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane; Receptor.		
FT FT SIGNAL 1 23 POTENTIAL.		
FT FT CHAIN 24 329 T LYMPHOCYTE ACTIVATION ANTIGEN CD86.		
FT FT DOMAIN 24 247 EXTRACELLULAR (POTENTIAL).		
FT FT TRANSMEM 248 268 POTENTIAL.		
FT FT DOMAIN 269 329 CYTOPLASMIC (POTENTIAL).		
FT FT DOMAIN 33 117 IG-LIKE V-TYPE DOMAIN.		
FT FT DOMAIN 149 225 IG-LIKE C2-TYPE DOMAIN.		
FT FT DISULFID 40 110 POTENTIAL.		
FT FT DISULFID 157 218 POTENTIAL.		
FT FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL).		
FT FT CARBOHYD 47 47 N-LINKED (GLCNAC. . .) (POTENTIAL).		
FT FT CARBOHYD * 135 N-LINKED (GLCNAC. . .) (POTENTIAL).		

RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RC MEDLINE=9803888; PubMed=9734811;  
RA Ishikawa K.-I.; Nagase T.; Suyama M.; Miyajima N.; Tanaka A.;  
RA Kotani H.; Nomura N.; Ohara O.;  
RT Prediction of the coding sequences of unidentified human genes. X.  
RT The complete sequences of 100 new cDNA clones from brain which can  
code for large proteins in vitro.";  
RL DNA Res. 5;169-176(1998).  
RN [5]  
RP SEQUENCE FROM N.A. (ISOFORM 2).  
RA Ling V.; Danussi-Joannopoulos K.;  
RL Patent number WO0121796, 29-MAR-2001.  
CC -1- FUNCTION: LIGAND FOR THE T-CELL SPECIFIC CELL SURFACE RECEPTOR  
CC ICOS. ACTS AS A COSTIMULATORY SIGNAL FOR T-CELL PROLIFERATION AND  
CC CYTOKINE SECRETION; INDUCES ALSO B-CELL PROLIFERATION AND  
CC DIFFERENTIATION INTO PLASMA CELLS. COULD PLAY AN IMPORTANT ROLE IN  
CC MEDIATING LOCAL TISSUE RESPONSES TO INFLAMMATORY CONDITIONS, AS  
CC WELL AS IN MODULATING THE SECONDARY IMMUNE RESPONSE BY CO-  
CC STIMULATING MEMORY T-CELL FUNCTION (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).  
CC -1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; 1 (SHOWN HERE) AND 2;  
CC ARE PRODUCED BY ALTERNATIVE SPLICING.  
CC -1- TISSUE SPECIFICITY: ISOFORM 1 IS WIDELY EXPRESSED (BRAIN, HEART,  
CC KIDNEY, LIVER, LUNG, PANCREAS, PLACENTA, SKELETAL MUSCLE, BONE,  
CC MARROW, COLON, OVARY, PROSTATE, TESTIS, LYMPH NODES, LEUKOCYTES,  
CC SPLIEN, THYMUS AND TONSIL), WHILE ISOFORM 2 IS DETECTED ONLY IN  
CC LYMPH NODES, LEUKOCYTES AND SPLEEN.  
CC -1- INDUCTION: CONSTITUTIVE EXPRESSION IS FURTHER ENHANCED BY  
CC TREATMENT WITH TNF-ALPHA IN PERIPHERAL BLOOD B-CELLS AND  
CC MONOCYTES, WHILE IT IS DECREASED IN DENDRITIC CELLS.  
CC -1- SIMILARITY: CONTAINS 1 C2-LIKE DOMAIN.  
CC -1- SIMILARITY: CONTAINS 1 V-LIKE DOMAIN.  
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.  
CC -1- SUBFAMILY.  
CC -1- CAUTION: REF. 4 SEQUENCE DIFFERS FROM THAT SHOWN IN POSITION 300  
CC ONWARD FOR AN UNKNOWN REASON.

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CC EMBL: AF199038; AAF34739.1; -.  
DR EMBL: AF289028; AAG01176.1; -.  
DR EMBL: AF216749; AAK16241.1; -.  
DR EMBL: AB014533; BAA31628.1; ALT\_SEQ.  
DR MIM: 605717; -.  
DR InterPro: IPR003559; Ig.  
DR InterPro: IPR003006; Ig\_MHC.  
DR Pfam: PF00047; Ig.  
DR SMART: SM00409; Ig\_1.  
DR B-cell activation; Immune response; Glycoprotein;  
KW Immunoglobulin domain; Signal; Transmembrane; Multigene family;  
KW Alternative splicing.  
FT SIGNAL 1 18 POTENTIAL.  
FT DOMAIN 19 302 ICOS LIGAND.  
FT DOMAIN 19 256 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 257 277 POTENTIAL.  
FT DOMAIN 278 302 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 30 120 Ig-LIKE V-TYPE DOMAIN.  
FT DOMAIN 151 223 Ig-LIKE C2-TYPE DOMAIN.  
FT DISULFID 37 113 POTENTIAL.  
FT DISULFID 158 216 POTENTIAL.  
FT CARBOHYD 70 70 N-LINK (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 137 137 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 173 173 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 186 186 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 225 225 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT VARSPLIC 300 302 GHV->ESWNLLLILS (IN ISOFORM 2).  
SQ SEQUENCE 302 AA; 33349 MW; 64794AE21B5E34A CRC64;

Query Match 14.0%; Score 161; DB 1; Length 302;  
Best Local Similarity 26.4%; Pred. No. 1..6e-06;  
Matches 57; Conservative 36; Mismatches 95; Indels 28; Gaps 8;

Qy 14 KEVKEV ---ATLSCG-HNVSVEELAQTRIVWQ-KENKVKLT---MSGDMNIWPEYKN 63  
Db 23 KEVRAYVGSDVELSACAPEGSFRDNDVYYWQTSSEKTVYHQPNSLLENVDSRYRN 82

Qy 64 RTIEDF---ITNLNLSTVLAIRPSDECTYECVVKYKEVDAFKREHLAETVLSVKADPTP 119  
Db 83 RALMSPAGMLRQDFSLSLFNLNTVTPQDEKFHCVLVL-QSLGQEVLSVTILVAANFSVP 141

Qy 120 SISDFEPLTSNURRICGSTGGFPPEPHSWLЕНГЕЕЛНАИТВСОДЕТЕ-----L 171  
Db 142 VVSAPHSPSQDQLTFTSINGYPRPNVWINKTD----NSLQLAQNDTFLNMRGL 196

Qy 172 YAVSSKLDFNMTTNHSWCLIKYGHFLRVNQOPENWNT 207  
Db 197 YDVSVSURIARTPSVNGCCTENVLLQQLTVGSQT 232

RESULT 6  
CD86\_MOUSE STANDARD PRT; 309 AA.  
ID CD86\_MOUSE STANDARD; PRT; 309 AA.  
AC P42082;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE T LYMPHOCYTE ACTIVATION ANTIGEN CD86 PRECURSOR (ACTIVATION B7-2  
DE ANTIGEN) (EARLY T CELL COSTIMULATORY MOLECULE-1) (ETC-1).  
GN C086.  
OS Mus musculus (Mouse).  
OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Muridae; Murinae; Muridae; Sciurognathii; Muridae; Murinae; Mus.  
RN NCBI\_TAXID=10090;  
RN SEQUENCE FROM N.A.  
RN SEQUENCE FROM N.A.  
RX MEDLINE=94005585; PubMed=7504059;  
RA Freeman G.J., Borriello F., Hoddes R.J., Reiser H., Gibben J.G.,  
RA Goldberg J.M., Lombard G., Laszlo G., Lombard L.A.,  
RA Wang S., Gray G.S., Nadler L.M., Hatchcock K.,  
RA "Murine B7-2, an alternative CTLA4 counter receptor that costimulates  
RT T cell proliferation and interleukin 2 production.";  
RL J. Exp. Med. 178:2185-2192(1993).  
RN [2].  
RP SEQUENCE FROM N.A.  
RN SEQUENCE OF 7-309 FROM N.A.  
RX MEDLINE=94230971; PubMed=7499829;  
RA Chen C., Gault A., Shen L., Nabavi N.;  
RT "Molecular cloning and expression of early T cell costimulatory  
molecule-1 and its characterization as B7-2 molecule.";  
RL J. Immunol. 152:4949-4956(1994).  
RN [3].  
RP SEQUENCE OF 7-309 FROM N.A.  
RX MEDLINE=96094437; PubMed=96094437;  
RA Oliveros J., Freeman G.J., Nadler L.M., Sharpe A.H.;  
RT "Differential expression of alternate mb7-2 transcripts.";  
RL J. Immunol. 155:5490-5497(1995).  
RN [4].  
RP SEQUENCE OF 7-309 FROM N.A.  
RX MEDLINE=94230971; PubMed=7513726;  
RA Chen C., Gault A., Shen L., Nabavi N.;  
RT "Function: receptor involved in the costimulatory signal essential  
for T lymphocyte proliferation and interleukin 2 production, by  
binding CD28 or CTLA-4. May play a critical role in the early  
events of T cell activation and costimulation of naïve T cells,  
such as deciding between immunity and anergy that is made by T  
cells within 24 hours after activation."  
CC -1- FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL  
FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION, BY  
BINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY  
EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAÏVE T CELLS,  
SUCH AS DECIDING BETWEEN IMMUNITY AND ANERGY THAT IS MADE BY T  
CELLS WITHIN 24 HOURS AFTER ACTIVATION.  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -1- TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS.  
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS  
ONE C2-LIKE AND ONE V-LIKE DOMAINS.



CC	-!- TISSUE SPECIFICITY: ISOFORM 1 HIGHEST EXPRESSION IN LYMPHOID TISSUES, SUCH AS SPLEEN (MOSTLY IN THE MARGINAL ZONE), LYMPH NODES (PARTICULARLY IN THE CORTEX AND IN BOTH PRIMARY AND SECONDARY FOLLICLES), THYMUS (PREDOMINANTLY IN THE MEDULLA) AND PEYER'S PATCHES (MOSTLY IN THE FOLLICLES), LOWER LEVELS IN MANY NONLYMPHOID TISSUES, SUCH AS BRAIN, HEART, KIDNEY, LIVER, LONG SKELETAL MUSCLE AND TESTIS. PRESENT ON FRESHLY ISOLATED SPLENIC B-CELLS, T-CELLS, DENDRITIC CELLS AND MACROPHAGES. THE EXPRESSION OF ISOFORM 2 IS RESTRICTED TO HEART, SPLEEN AND KIDNEY.	Db	93 PYKSPGIVNDSSYKRNQHLSLDSMKQGNFSLYLKNTVPODTQEFCRV - FMNTATELVK 150
CC	-!- DEVELOPMENTAL STAGE: DETECTED EARLY IN HEMOPOTOCYTE; IN THE YOLK SAC AT 11.5 AND 12.5 DPC AND, TO A LESSER EXTENT, IN THE LIVER AT 14.5 DPC.	Qy	105 LAE--VTLVKADFPPP--SISDFELPTSNTRIICSTSGGPEPHISWLENGEELNAIN 160
CC	-!- SIMILARITY: CONTAINS 1 C2-LIKE DOMAIN.	Db	151 ILEEVYRLVRAANFSTPVISDSSNPGQE RTYICMSKNGYPEPNVYWI NTDNSLID 208
CC	-!- SIMILARITY: CONTAINS 1 V-LIKE DOMAIN.	Qy	161 TTVDSDP---ETELVYASSKLDENFTNHSFMCLIKYHLRVN --- QTWNNTTK 209
CC	-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.	Db	209 TALQNNIVYLNLGLYDVISTLRLPWTSRGDVLCVENVALHQNTISQSRESFTNTK 268
CC	-!- SIMILARITY: CONTAINS 1 V-LIKE DOMAIN.	RESULT 8	
CC	-!- SIMILARITY: SUBFAMILY.	CD86_RABBIT	STANDARD;
CC	-!- This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and thus its statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).	ID	CB86_RABBIT
CC	-!- EMBL; AF216747; AAF45149_1; DR	AC	P42071;
CC	-!- EMBL; AF1199027; AAF34738_1; DR	DT	01-NOV-1995 (Rel. 32, Created)
CC	-!- EMBL; AX100591; CAC36463_1; DR	DT	01-OCT-1995 (Rel. 32, Last sequence update)
CC	-!- EMBL; AX100593; CAC36464_1; DR	DT	01-OCT-1996 (Rel. 34, Last annotation update)
CC	-!- MGI; 1354701; Icos1.	DE	B LYMPHOCYTE ACTIVATION ANTIGEN CD86 PRECURSOR (ACTIVATION B7-2 ANTIGEN).
CC	-!- InterPro: IPR003599; Ig_	DE	Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecules.
CC	-!- DR	GN	RT Immunogenetics 42:217-220(1995)
CC	-!- DR	RN	SEQUENCE FROM N.A.
CC	-!- DR	RP	SPRAIN-B/J X CHB/HM; PubMed=7642234;
CC	-!- DR	RC	MEDLINE=9539849; PubMed=7642234;
CC	-!- DR	RA	Iscone T., Seto A.;
CC	-!- DR	RT	*Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecules.
CC	-!- DR	RL	RT Immunogenetics 42:217-220(1995)
CC	-!- DR	CC	-!- FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION, BY BINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NATIVE T CELLS, SUCH AS DECIDING BETWEEN IMMUNITY AND ANERGY THAT IS MADE BY T CELLS WITHIN 24 HOURS AFTER ACTIVATION.
CC	-!- DR	CC	-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS ONE C2-LIKE AND ONE V-LIKE DOMAINS.
CC	-!- DR	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and thus its statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).
CC	-!- DR	CC	DR EMBL: D49842; BAA08642_1; -
CC	-!- DR	DR	InterPro: IPR003006; Ig_MHC.
CC	-!- DR	DR	InterPro: IPR003516; Ig_V.
CC	-!- DR	DR	SMART: SM00406; Ig_V.
CC	-!- DR	DR	PROSITE: PS00290; Ig_MHC; 1; POTENTIAL.
CC	-!- DR	KW	Immunoglobulin domain; Signal; Transmembrane; Multigene family; KW Alternative splicing.
CC	-!- FT	FT	BY SIMILARITY.
CC	-!- FT	CHAIN	1 46 ICOS LIGAND.
CC	-!- FT	DOMAIN	47 322 EXTRACELLULAR (POTENTIAL).
CC	-!- FT	TRANSMEM	47 277 POTENTIAL.
CC	-!- FT	DOMAIN	278 298 CTOPLASMIC (POTENTIAL).
CC	-!- FT	DOMAIN	299 322 IG-LIKE V-TYPE DOMAIN.
CC	-!- FT	DOMAIN	55 145 IG-LIKE C2-TYPE DOMAIN.
CC	-!- FT	DOMAIN	178 250 POLY-LEU.
CC	-!- FT	DOMAIN	31 38 POLY-ALA.
CC	-!- FT	DISULFID	289 292 POTENTIAL.
CC	-!- FT	DISULFID	62 138 POTENTIAL.
CC	-!- FT	DISULFID	185 243 POTENTIAL.
CC	-!- FT	CARBOHYD	71 71 N-LINKED (GLCNAC . . ) (POTENTIAL).
CC	-!- FT	CARBOHYD	120 120 N-LINKED (GLCNAC . . ) (POTENTIAL).
CC	-!- FT	CARBOHYD	163 163 N-LINKED (GLCNAC . . ) (POTENTIAL).
CC	-!- FT	CARBOHYD	200 200 N-LINKED (GLCNAC . . ) (POTENTIAL).
CC	-!- FT	CARBOHYD	213 213 N-LINKED (GLCNAC . . ) (POTENTIAL).
CC	-!- FT	CARBOHYD	252 252 N-LINKED (GLCNAC . . ) (POTENTIAL).
CC	-!- FT	CARBOHYD	265 265 N-LINKED (GLCNAC . . ) (POTENTIAL).
CC	-!- FT	CARBOHYD	321 322 HA -> TWAPVPQDYLIPRYLMSPCLKTRGLP (IN ISOFORM 2).
CC	-!- FT	VARSPLIC	R -> H (IN REF. 4 AND 5; CAC36464 ).
CC	-!- SQ	SEQUENCE	237 237 R -> H (IN REF. 4 AND 5; CAC36464 ).
CC	-!- SQ	SEQUENCE	322 35960 AA; MW; 55CCBA4AD12E47E6 CRC64.
Query Match	13.1%	Score 150.5; DB 1; Length 322;	POTENTIAL.
Best Local Similarity	27.1%	Pred. No. 1..3e-05; Mismatches 102; Indels 41; Gaps 12;	IG-LIKE V-TYPE DOMAIN.
Matches	65;	Conservative	IG-LIKE C2-TYPE DOMAIN.
Qy	2 LSHEFC--SGVHYTKVEKAVATLSCGHNVSE----ELAQTRIYQKEKKM-----L 48	POTENTIAL.	N-LINKED (GLCNAC. . . ) (POTENTIAL).
Db	38 LSSCICAAASAEETVGAMVGSNNVLSC----IDPHRRHFNGLYVQIQENPEVSVTYL 92	POTENTIAL.	N-LINKED (GLCNAC. . . ) (POTENTIAL).
Qy	49 TMMSGDMNTWPEYKNRTIDTN---NLSIVTLARPSDEGTIECVVLYKEFDAFREH 104	POTENTIAL.	N-LINKED (GLCNAC. . . ) (POTENTIAL).

FT	CARBOHYD	192	192	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	198	198	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	213	213	N-LINKED (GLCNAC. . .) (POTENTIAL).	
SQ	SEQUENCE	330 AA;	37142 MW;	935CD65C57E3EE1 CRC64;	
Query Match		12.28;	Score 140.5; DB 1;	Length 330;	
Best Local Similarity	27.48%; Pred. No. 9.4e-05;				
Matches	60; Conservative	34; Mismatches	84; Indels	41; Gaps	12;
QY	18	EVATLSCGH-NYSVEELAQTTRIYWOKEKKMVLTTM---SGMMNITPEYKNTTIDTN-	71		
Db	34	KPADLPCOFTNSQSRSLSLEVYWDQERLYLXFLGREKDPDNVDRKYIGTSFDOESW	93		
QY	72	NLSIVITALRPSDEGTVECVVLYKEKDAFKRHLAEVTLSVKADEFPTPSISFEIPHSNI	131		
Db	94	NLQLHNVQIK--DKGIVYQCFVHRAKGVLVPIQMNSELSTLVANFQPEIT---LISNI	147		
QY	132	RR----LICSTGGFPBPFLHSEELAINNTY-----SOPDETELY--AVSS	176		
Db	148	TRNSAINLTCSVSYQGPKMKFF---VLTENATEYDGVIKEKSDDNVGTLVNTSISG	203		
QY	177	KLD芬-NMTTNHSMCLIKYGHLRVNOTEWNNTKQEHFF	214		
Db	204	SITFSDDIRNATIYCVL-----QTESTEVYSS-Q-HFF	233		
RESULT	9				
Cl66_MOUSE					
TD	C166_MOUSE_070136; STANDARD;	PRT;	583 AA.		
AC	Q61490-070136;				
DR	01-NOV-1997 (Rel. 35, Created)				
DR	15-JUL-1999 (Rel. 38, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	CD166 ANTIGEN PRECURSOR (ACTIVATED LEUKOCYTE-CELL ADHESION MOLECULE)				
DE	(ALCAM) (DM GRASP PROTEIN).				
GN	ALCAM.				
OS	Mus musculus (Mouse).				
OC	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
RN	[1]				
RN	NCBI_TAXID=10090;				
RP	SEQUENCE FROM N_A.				
RC	STRAIN=NFS;				
RX	MEMLIN#97353242; PubMed#9209500;				
RA	Bowen M.A., Bajjath J., D'Eglio M., Whitney G.S., Palmer D.,				
RA	Kobarg J.J., Starling G.C., Siadak A.W., Aruffo A.;				
RA	"Characterization of mouse ALCAM (Cpn166); the CD6 binding domain is conserved in different homologs and mediates cross-species binding."				
RA	Eur. J. Immunol. 27:1469-1478(1997).				
RN	[2]				
RP	SEQUENCE OF 227-583 FROM N_A.				
RC	STRAIN=BALB/C; TISSUE=Brain;				
RX	MEMLIN#943760B; PubMed#809660;				
RA	Kanki J.-P., Chang S., Kuvada J.Y.				
RT	"The molecular cloning and characterization of potential chick				
RT	DM-GRASP homologs in chicken and mouse."				
RL	J. Neurobiol. 25:831-845(1994).				
CC	- FUNCTION: CELL ADHESION MOLECULE THAT BINDS TO CD6. INVOLVED IN NEURITE EXPANSION BY NEURONS VIA HETEROPHILIC AND HOMOPHILIC INTERACTIONS. MAY PLAY A ROLE IN THE BINDING OF T AND B CELLS TO ACTIVATED LEUKOCYTES, AS WELL AS IN INTERACTIONS BETWEEN CELLS OF THE NERVOUS SYSTEM.				
CC	- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.				
CC	- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS 3 C2-LIKE AND 2 V-LIKE DOMAINS.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).				
CC	or send an email to license@isb-sib.ch).				
CC	CC	CC	CC	CC	CC
DR	EMBL; L25274; AAA37528.1; -.				
DR	MGI; MG1:1311266; Alcam.				
DR	InterPro; IPR003599; Ig_MHC.				
DR	InterPro; IPR003600; Ig_Q-like.				
DR	Pfam; PF00047_19; 5.				
DR	SMART; SM00419; Ig; 3.				
DR	SMART; SM00410; Ig-like. 2.				
DR	PROSITE; PS00290; Ig_MHC; FALSE_NEG.				
KW	Cell adhesion; Immunoglobulin domain; Glycoprotein; Transmembrane; Signal.				
KW					
FT	SIGNAL	1	27		
FT	CHAIN	28	583		
FT	DONAIN	28	549		
FT	TRANSMEM	528	583		
FT	DOMAIN	550	583		
FT	DONAIN	263	321		
FT	DONAIN	347	399		
FT	DONAIN	428	492		
FT	DISULFID	43	113		
FT	DISULFID	157	220		
FT	DISULFID	270	313		
FT	DISULFID	354	392		
FT	DISULFID	435	485		
FT	CARBOHYD	95	95		
FT	CARBOHYD	167	167		
FT	CARBOHYD	265	265		
FT	CARBOHYD	306	306		
FT	CARBOHYD	361	361		
FT	CARBOHYD	457	457		
FT	CARBOHYD	480	480		
FT	CARBOHYD	499	499		
FT	CONFFLICT	227	232		
FT	CONFFLICT	454	454		
SEQUENCE	583 AA;	65161 MW;	E7BAFF8FCAB9489 CRC64;		
Query Match					
Best Local Similarity	11.7%	Score 134.5; DB 1; Length 583;			
Matches	38; Conservative	Pred. No. 0.0061;			
Mismatches	34; Mismatches	54; Indels	25; Gaps	7;	
QY	59 PEYKNRTIFDITNNLSLVILALRPSDEGYECVVLKVEKDARKHLEAVTLSVKADPFT 118				
Db	84 PEYKDR--LTSLSSENVTLSANAKISDEKFREKMLVLT-EDNFYFEAPTLVKV-----FKQ 133				
QY	119 PSISDFB-----IPTSNIRRI--ICSTSGFPFPFLSWLNGEELNATNTVS-----OD 166				
Db	134 PSKPEIVNKAPFLETDLKLKGDC1SRSYDPGNTIWYRNGKVLQPVEGEVALLFKIED 193				
QY	167 PETELYAVSSKLDNFMTNH--SFMCILKY 194				
Db	194 PGQLYTVSSLEYKTTRSDIQMPFTCSVTY 224				
RESULT	10				
C166_HUMAN					
ID	C166_HUMAN STANDARD;				
AC	Q13740; 060892;				
DT	01-NOV-1997 (Rel. 35, Created)				
DT	01-NOV-1997 (Rel. 35, Last sequence update)				
DT	20-AUG-2001 (Rel. 40, Last annotation update)				
DE	CD166 ANTIGEN PRECURSOR (ACTIVATED LEUKOCYTE-CELL ADHESION MOLECULE)				
DE	(ALCAM), ALCAM, ALCAM OR MEM.				
GN	Homo sapiens (Human).				
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
CC	Mammalia; Buttoes; Primates; Catarrhini; Hominidae; Homo.				
CC	NCBIX TAXID=9606;				
CC	[1] SEQUENCE FROM N_A.				



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 CC or send an email to license@isb-sib.ch).

CC -----

CC EMBL; VO1555; CAA24809\_1; -.

CC PIR; A03192; Q00E48.

CC PIR; S3\_058; S33058.

CC InterPro; IPR003600; Ig-like.

CC SMART; SM00410; Ig-like; 1.

CC EARLY protein; transforming protein.

CC KW Early protein; transforming protein.

CC SQ SEQUENCE 221 AA; 24471 MW; C5A2AD1EA28758E CRC64;

CC -----

Query Match 11.28; Score 129; DB 1; Length 221;

Best Local Similarity 27.0%; Conservative 25; Pred. No. 0.00052; Gaps 8;

Matches 43; Conservative 47; Indels 44; Gaps 8;

Qy 18 EVATLSCGHNSVVEELAQTRIYWK-----EKKAVYLTMNSGDMNIWPE 60

Db 19 QAVTAFLGERTVLT-----WRRVSLGPEIEVSNEFKLGPPQEQLIGRMHHDV-TFIE 71

Qy 61 YKMRITFDI--TNNLSTIVILALRPSDEGTYCIVVLYKEDAFKREHLAEV--TLSV-- 112

Db 72 WPERGEFTDIIHRASNTTFLVVTANISHDGNYLCRMKGTEVTKOEHLSVVKPLTLSVHS 131

Qy 113 -KADFEPTPSISDEPIPSNIRRICSTSGGFEPHLSWL 150

Db 132 ERSQFP-----DEFSLT-----VTCVNNAFFPHYQWL 159

## RESULT 12

BUTY\_HUMAN ID BUTY\_HUMAN STANDARD; PRT; 526 AA.

AC Q13410 [1]

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE BUTYROPHILIN PRECURSOR (BT).

GN BTN1A1 OR BTN.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

RN [1] NCBI\_TaxID=9606;

RP SEQUENCE FROM N.A.

RC TISSUE-Breast;

RX MEDLINE=96-201696; PubMed=8611614;

RA Taylor M.R.; Peterson J.A.; Ceriono R.L.; Couto J.R.;

RP "Cloning and sequence analysis of human butyrophilin reveals a

potential receptor function".

RL Biochim. Biophys. Acta 1306:1-4 (1996).

CC -1- FUNCTION: MAY ACT AS A SPECIFIC MEMBRANE ASSOCIATED RECEPTOR FOR THE MILK-FAT DROPLETS. IT

ASSOCIATION OF CITOPLASMIC DROPLETS WITH THE APICAL PLASMA

MEMBRANE (BY SIMILARITY).

CC -1- SUBUNIT: SEEEMS TO ASSOCIATE WITH XANTHINE DEHYDROGENASE/OXIDASE

(BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS 1

V-LIKE DOMAIN. BELONGS TO THE BTN/MOG SUBFAMILY.

CC -1- SIMILARITY: STRONG, TO THE C-TERMINAL OF RET FINGER PROTEIN (RFP).

CC -----

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or send an email to license@isb-sib.ch).

CC EMBL; U39576; AAC50489.1; -

DR MIM: 601610; -

DR InterPro; IPR003879; Butyroph-DUF-C.

DR InterPro; IPR001870; Gamma\_carboxylise.

CC InterPro; IPR003006; Ig-MHC.

CC InterPro; IPR003596; Ig-V.

CC InterPro; IPR003877; SPRY.

CC Pfam; PF00044; Ig-1.

CC Pfam; PF00622; SPRY; 1.

CC SMART; SM00446; Ig-V.

CC SMART; SM00449; SPRY; 1.

CC KW Transmembrane; Glycoprotein; Immunoglobulin domain; signal.

CC SQ SIGNAL BY SIMILARITY.

CC BUTYROPHILIN.

CC EXTRACELLULAR (POTENTIAL).

CC POTENTIAL.

CC CYTOPLASMIC (POTENTIAL).

CC N-LINKED (GLCNAC).

CC (POTENTIAL).

CC N-LINKED (GLCNAC).

CC (POTENTIAL).

CC SEQUENCE 526 AA; 59004 MW; E9ECA0CF8DAF94D5 CRC64;

CC -----

Query Match 11.28; Score 127; DB 1; Length 526;

Best Local Similarity 27.5%; Pred. No. 0.0023; Gaps 10;

Matches 52; Conservative 33; Mismatches 84; Indels 20; Gaps

52; Standard; PRT; 526 AA.

Query Match 11.18; Score 127; DB 1;

Best Local Similarity 27.5%; Pred. No. 0.0023;

Matches 52; Conservative 33; Mismatches 84; Indels 20; Gaps

52; Standard; PRT; 526 AA.

Query Match 11.18; Score 127; DB 1;

Best Local Similarity 27.5%; Pred. No. 0.0023;

Matches 52; Conservative 33; Mismatches 84; Indels 20; Gaps

52; Standard; PRT; 526 AA.

Query Match 11.18; Score 127; DB 1;

Best Local Similarity 27.5%; Pred. No. 0.0023;

Matches 52; Conservative 33; Mismatches 84; Indels 20; Gaps

52; Standard; PRT; 526 AA.

Query Match 11.18; Score 127; DB 1;

Best Local Similarity 27.5%; Pred. No. 0.0023;

Matches 52; Conservative 33; Mismatches 84; Indels 20; Gaps

52; Standard; PRT; 526 AA.

Query Match 11.18; Score 127; DB 1;

Best Local Similarity 27.5%; Pred. No. 0.0023;

Matches 52; Conservative 33; Mismatches 84; Indels 20; Gaps

52; Standard; PRT; 526 AA.

Query Match 11.18; Score 127; DB 1;

Best Local Similarity 27.5%; Pred. No. 0.0023;

Matches 52; Conservative 33; Mismatches 84; Indels 20; Gaps

52; Standard; PRT; 526 AA.

Query Match 11.18; Score 127; DB 1;

Best Local Similarity 27.5%; Pred. No. 0.0023;

Matches 52; Conservative 33; Mismatches 84; Indels 20; Gaps

52; Standard; PRT; 526 AA.

Query Match 11.18; Score 127; DB 1;

Best Local Similarity 27.5%; Pred. No. 0.0023;

Matches 52; Conservative 33; Mismatches 84; Indels 20; Gaps

52; Standard; PRT; 526 AA.

Query Match 11.18; Score 127; DB 1;

Best Local Similarity 27.5%; Pred. No. 0.0023;

Matches 52; Conservative 33; Mismatches 84; Indels 20; Gaps

52; Standard; PRT; 526 AA.

Query Match 11.18; Score 127; DB 1;

Best Local Similarity 27.5%; Pred. No. 0.0023;

Matches 52; Conservative 33; Mismatches 84; Indels 20; Gaps

52; Standard; PRT; 526 AA.

Query Match 11.18; Score 127; DB 1;

Best Local Similarity 27.5%; Pred. No. 0.0023;

Matches 52; Conservative 33; Mismatches 84; Indels 20; Gaps

52; Standard; PRT; 526 AA.

Query Match 11.18; Score 127; DB 1;

Best Local Similarity 27.5%; Pred. No. 0.0023;

Matches 52; Conservative 33; Mismatches 84; Indels 20; Gaps

52; Standard; PRT; 526 AA.

Query Match 11.18; Score 127; DB 1;

Best Local Similarity 27.5%; Pred. No. 0.0023;

Matches 52; Conservative 33; Mismatches 84; Indels 20; Gaps

52; Standard; PRT; 526 AA.

Query Match 11.18; Score 127; DB 1;

Best Local Similarity 27.5%; Pred. No. 0.0023;

Matches 52; Conservative 33; Mismatches 84; Indels 20; Gaps

52; Standard; PRT; 526 AA.

Query Match 11.18; Score 127; DB 1;

Best Local Similarity 27.5%; Pred. No. 0.0023;

Matches 52; Conservative 33; Mismatches 84; Indels 20; Gaps

52; Standard; PRT; 526 AA.

Query Match 11.18; Score 127; DB 1;

Best Local Similarity 27.5%; Pred. No. 0.0023;

Matches 52; Conservative 33; Mismatches 84; Indels 20; Gaps

52; Standard; PRT; 526 AA.

Query Match 11.18; Score 127; DB 1;

Best Local Similarity 27.5%; Pred. No. 0.0023;

Matches 52; Conservative 33; Mismatches 84; Indels 20; Gaps

52; Standard; PRT; 526 AA.

Query Match 11.18; Score 127; DB 1;

Best Local Similarity 27.5%; Pred. No. 0.0023;

Matches 52; Conservative 33; Mismatches 84; Indels 20; Gaps

52; Standard; PRT; 526 AA.

Query Match 11.18; Score 127; DB 1;

Best Local Similarity 27.5%; Pred. No. 0.0023;

Matches 52; Conservative 33; Mismatches 84; Indels 20; Gaps

52; Standard; PRT; 526 AA.

Query Match 11.18; Score 127; DB 1;

Best Local Similarity 27.5%; Pred. No. 0.0023;

Matches 52; Conservative 33; Mismatches 84; Indels 20; Gaps

52; Standard; PRT; 526 AA.

Query Match 11.18; Score 127; DB 1;

Best Local Similarity 27.5%; Pred. No. 0.0023;

Matches 52; Conservative 33; Mismatches 84; Indels 20; Gaps

52; Standard; PRT; 526 AA.

Query Match 11.18; Score 127; DB 1;

Best Local Similarity 27.5%; Pred. No. 0.0023;

Matches 52; Conservative 33; Mismatches 84; Indels 20; Gaps

52; Standard; PRT; 526 AA.

Query Match 11.18; Score 127; DB 1;

Best Local Similarity 27.5%; Pred. No. 0.0023;

Matches 52; Conservative 33; Mismatches 84; Indels 20; Gaps

52; Standard; PRT; 526 AA.

Query Match 11.18; Score 127; DB 1;

Best Local Similarity 27.5%; Pred. No. 0.0023;

Matches 52; Conservative 33; Mismatches 84; Indels 20; Gaps

52; Standard; PRT; 526 AA.

Query Match 11.18; Score 127; DB 1;

Best Local Similarity 27.5%; Pred. No. 0.0023;

Matches 52; Conservative 33; Mismatches 84; Indels 20; Gaps

52; Standard; PRT; 526 AA.

Query Match 11.18; Score 127; DB 1;

Best Local Similarity 27.5%; Pred. No. 0.0023;

Matches 52; Conservative 33; Mismatches 84; Indels 20; Gaps

52; Standard; PRT; 526 AA.

Query Match 11.18; Score 127; DB 1;

Best Local Similarity 27.5%; Pred. No. 0.0023;

Matches 52; Conservative 33; Mismatches 84; Indels 20; Gaps

52; Standard; PRT; 526 AA.

Query Match 11.18; Score 127; DB 1;

Best Local Similarity 27.5%; Pred. No. 0.0023;

Matches 52; Conservative 33; Mismatches 84; Indels 20; Gaps

52; Standard; PRT; 526 AA.

Query Match 11.18; Score 127; DB 1;

Best Local Similarity 27.5%; Pred. No. 0.0023;

Matches 52; Conservative 33; Mismatches 84; Indels 20; Gaps

52; Standard; PRT; 526 AA.

Query Match 11.18; Score 127; DB 1;

Best Local Similarity 27.5%; Pred. No. 0.0023;

Matches 52; Conservative 33; Mismatches 84; Indels 20; Gaps

52; Standard; PRT; 526 AA.

Query Match 11.18; Score 127; DB 1;

Best Local Similarity 27.5%; Pred. No. 0.0023;

Matches 52; Conservative 33; Mismatches 84; Indels 20; Gaps

52; Standard; PRT; 526 AA.

Query Match 11.18; Score 127; DB 1;

Best Local Similarity 27.5%; Pred. No. 0.0023;

Matches 52; Conservative 33; Mismatches 84; Indels 20; Gaps

52; Standard; PRT; 526 AA.

Query Match 11.18; Score 127; DB 1;

Pourquier O., Corbel C., le Caer J.-P., Rossier J., le Douarin N.M.;  
 RT "BEN," a surface glycoprotein of the immunoglobulin superfamily, is  
 expressed in a variety of developing systems.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:5261-5265(1992).  
 [4]

RP POSSIBLY FUNCTION. MEDLINE=92211411; PubMed=1313497;

RA Pourquier O., Hallonet M.F.R., le Douarin N.M.;  
 RT "Association of BEN glycoprotein expression with climbing fiber  
 axogenesis in the avian cerebellum.";  
 RL J. Neurosci. 12:1548-1557(1992).

-!- POSITION: HOMOPHILIC ADHESION MOLECULE ASSOCIATED WITH CLIMBING  
 FIBER AXONOPHILIC SUPPORTS NEURITE EXTENSION.

CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -!- TISSUE SPECIFICITY: EXPRESSED IN A RESTRICTED POPULATION OF AXONS.  
 CC WITHIN THE SPINAL CORD IT IS LOCALIZED TO AXONS IN THE DORSAL  
 FUNICULUS, MIDLINE FLOOR PLATE CELLS, AND MOTONEURONS. FOUND IN  
 CC EPITHELIA, CENTRAL NERVOUS SYSTEM, AND HEMOPOIETIC CELLS. EACH  
 CC DEVELOPING SYSTEM CARRIES DIFFERENTLY GLYCOSYLATED MOLECULAR FORMS  
 OF BEN.

CC -!- DEVELOPMENTAL STAGE: WIDELY EXPRESSED DURING EMBRYONIC  
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS  
 CC 3 C2-LIKE AND 2 V-LIKE DOMAINS.

CC -----

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 or send an email to license@isb-sib.ch).

CC CDR EMBL; S63276; ABB20170.1; .  
 CC CDR EMBL; M76678; AAA48602.1; .  
 CC CDR EMBL; X64301; CAA45579.1; .  
 CC HSSP; Q13740; 1KJC.  
 CC InterPro; IPR003599; 19.  
 CC InterPro; IPR003600; Ig-like.  
 CC InterPro; IPR003006; 19 MHC.  
 CC InterPro; IPR0047; 19; 5.  
 CC SMART; SM00409; Ig; 3.  
 CC SMART; SM00410; Ig-like; 2.  
 CC PROSITE; PS00290; Ig MHC; FALSE NEG.  
 KW Cell adhesion; Immunoglobulin domain; Glycoprotein; Transmembrane  
 KW signal.

FT SIGNAL 1 33 CD166 ANTIGEN. CD166 ANTIGEN. CD166 ANTIGEN.  
 FT CHAIN 34 588 EXTRACELLULAR (POTENTIAL). EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 34 532 POTENTIAL. POTENTIAL.  
 FT TRANSMEM 533 553 CYTOPLASMIC (POTENTIAL). CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 554 588 IG-LIKE V-TYPE DOMAIN 1. IG-LIKE V-TYPE DOMAIN 1.  
 FT DOMAIN 42 126 IG-LIKE V-TYPE DOMAIN 2. IG-LIKE V-TYPE DOMAIN 2.  
 FT DOMAIN 156 233 IG-LIKE C2-TYPE DOMAIN 1. IG-LIKE C2-TYPE DOMAIN 1.  
 FT DOMAIN 269 326 IG-LIKE C2-TYPE DOMAIN 2. IG-LIKE C2-TYPE DOMAIN 2.  
 FT DOMAIN 352 404 IG-LIKE C2-TYPE DOMAIN 3.  
 FT DOMAIN 433 497  
 FT DISULFID 49 119  
 FT DISULFID 163 226  
 FT DISULFID 276 319  
 FT DISULFID 359 397  
 FT DISULFID 440 490  
 FT CARBOHYD 440 101  
 FT CARBOHYD 173 173  
 FT CARBOHYD 199 199  
 FT CARBOHYD 271 271  
 FT CARBOHYD 312 312  
 FT CARBOHYD 366 366  
 FT CARBOHYD 462 462  
 FT CARBOHYD 485 485  
 FT CARBOHYD 504 504  
 FT CONFLICT 2 10  
 FT CONFLICT 25 25  
 FT CONFLICT 112 113

FT CONFLICT 329 329 A -> T (IN REF. 2).  
 FT CONFLICT 401 402 LQ -> HK (IN REF. 2).  
 SQ SEQUENCE 588 AA; 65726 MW; 2A88612B0164331E CRC64;

Query Match Score 122.5; DB 1; Length 588;  
 Best Local Similarity 25.%; Pred. No. 0.0062;  
 Matches 39; Conservative 32; Mismatches 54; Indels 27; Gaps 8;

Qy 59 PEYKARTIFDTNNLSVIALRPSDEGTIVCVVLYKDAFKRPHLAEVTLYSVKADFP 118  
 Db 90 PDYKQR-LSUSENTYLTSKKNARISDEKRVCLMVT-EDDVSEPTVVKY------FKQ 139

Qy 119 PS-----ISDFEPISTNIRRI-IGSTGGFPPEHPSLWENG-----EEELNAINTTVSQ 165  
 Db 140 PSQPELTHQADF-LTEKLMGECVRDSPYEGNVTYKNGRVLQPVEVVVNLRKVE 198

Qy 166 DPETELYAVSSSKLDFNM-----TNHSFMCILKY 194  
 Db 149 NRSTGLFTMTSSLQYMPTEKANAKFTCIVY 230

RESULT 14  
 BUTY\_MOUSE STANDARD; PRT; 524 AA.  
 ID BUTY\_MOUSE ; STANDARD;  
 ID BUTY\_MOUSE ; PRT; 524 AA.  
 AC Q62556; P97392;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE BUTYROPHILIN PRECURSOR (BP).  
 GN BTN1AL OR BTN N.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TAXID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129; TISSUE=Mammary gland;  
 RX MEDLINE=97148936; PubMed=8095761;  
 RA Ogg S.L., Komaragiri M.V.S., Mather I.H.;  
 RT "Structural organization and mammary-specific expression of the  
 RT butyrophilin gene.";  
 RT Mamm. Genome 7:900-905 (1996).  
 RL RN [2]  
 RP SEQUENCE OF 39-487 FROM N.A.  
 RC TISSUE=Mammary gland;  
 RX MEDLINE=96125722; PubMed=8541302;  
 RA Ishii T., Aoki N., Nozaki A., Adachi T., Nakamura R., Matsuda T.;  
 RT "Carboxy-terminal cytoplasmic domain of mouse butyrophilin  
 specifically associates with a 150-kDa protein of mammary epithelial  
 cells and milk fat globule membrane."  
 RL Blochim. Biophys. Acta 1245:285-292 (1995).  
 CC -!- FUNCTION: MAY FUNCTION IN THE SECRETION OF MILK-FAT DROPLETS. IT  
 CC MAY ACT AS A SPECIFIC MEMBRANE-ASSOCIATED RECEPTOR FOR THE  
 CC ASSOCIATION OF CYTOPLASMIC DROPLETS WITH THE APICAL PLASMA  
 CC MEMBRANE (BY SIMILARITY).  
 CC -!- SUBUNIT: SEEMS TO ASSOCIATE WITH XANTHINE DEHYDROGENASE/OXIDASE.  
 CC -!- SUBCELLULAR LOCALIZATION: TYPE I MEMBRANE PROTEIN.  
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN MAMMARY TISSUE AND SECRETED IN  
 CC ASSOCIATION WITH THE MILK-FAT-GLOBULE MEMBRANE DURING LACTATION.  
 CC -!- DEVELOPMENTAL STAGE: EXPRESSION INCREASES DURING THE LAST HALF OF  
 CC PREGNANCY AND IS MAXIMAL DURING LACTATION.  
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS 1  
 CC V-LIKE DOMAIN. BELONGS TO THE BN/MOG SUBFAMILY.  
 CC -!- SIMILARITY: STRONG, TO THE C-TERMINAL OF RET FINGER PROTEIN (RFP).  
 CC -----

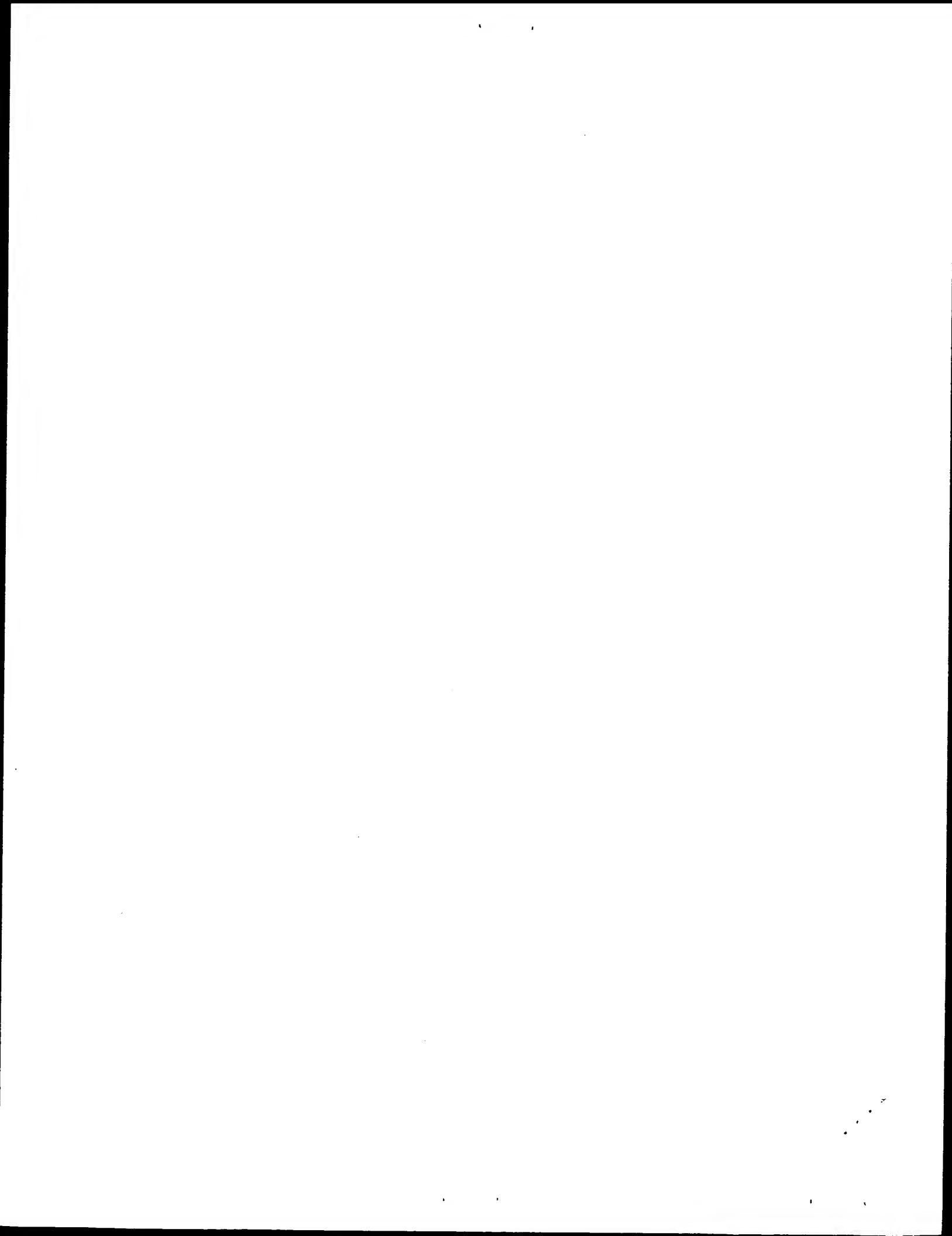
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CC	DR EMBL; U67065; AAB51034.1;	RA Krieg P.A., Sakaguchi D.S., Kintner C.R.;
DR	EMBL; SB8642; AAB35893.1;	"Primary structure and developmental expression of a large cytoplasmic domain form of <i>xenopus laevis</i> neural cell adhesion molecule (NCAM)."
DR	MGD; MGI:103118; Bntnl1	RT Nucleic Acids Res. 17:10321-10335(1989).
DR	InterPro; IPR001870; Butyroph_DUF_C.	-!- FUNCTION: THIS PROTEIN IS A CELL ADHESION MOLECULE INVOLVED IN NEURON-NEURON ADHESION, NEURITE FASCICULATION, OUTGROWTH OF NEURITES, ETC.
DR	InterPro; IPR001870; Gamma_carboxylse.	CC NEURITES, ETC.
DR	InterPro; IPR003006; Ig_MHC.	CC SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
DR	InterPro; IPR003556; Ig_v.	CC -!- ALTERNATIVE PRODUCTS: THE DIFFERENT TISSUE-SPECIFIC FORMS OF N-CAM ARE PRODUCED BY ALTERNATIVE SPLICING
DR	InterPro; IPR003877; SPRY.	CC -!- TISSUE SPECIFICITY: EXPRESSED IN NEURON AND IN PRESUMPTIVE NEURAL TISSUE.
DR	Pfam; PF00047; Ig_1.	CC -!- DEVELOPMENTAL STAGE: THE mRNA ENCODING THIS LD-NCAM IS THE MAJOR TRANSCRIPT PRESENT IN BOTH MATERNAL RNA AND IN THE EMBRYO DURING EARLY NEURAL DEVELOPMENT.
DR	Pfam; PF00622; SPRY; 1.	CC -!- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
SMART	SM00406; IgV; 1.	CC -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
SMART	SM00449; SPRY; 1.	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).
KW	Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.	CC -----
FT SIGNAL	1 26	CC -----
FT DOMAIN	27 524	CC -----
FT TRANSMEM	27 247	CC -----
FT DOMAIN	248 268	CC -----
FT CARBOHYD	269 524	CC -----
FT CARBOHYD	56 556	CC -----
FT CONFLICT	216 216	CC -----
FT CONFLICT	46 46	CC -----
FT CONFLICT	117 117	CC -----
FT CONFLICT	191 191	CC -----
FT CONFLICT	210 210	CC -----
FT CONFLICT	363 363	CC -----
FT CONFLICT	408 408	CC -----
FT CONFLICT	413 414	CC -----
FT CONFLICT	420 423	CC -----
FT CONFLICT	492 509	CC -----
SEQUENCE	524 AA:	58406 MW: 333FADE2C7/704480 CRC64;
Qy	20 ATLSCGH--NYSEEELAQTRIYQKEKKMVLTIMMSGD-----MNTNPEYKRN-----TIFD 68	Query Match Score 119; DB 1; Length 524;
Best Local Similarity	23.83%; Pred. No. 0.011;	
Matches	44; Conservative 34; Mismatches 87; Indels 20; Gaps 7;	
Db	47 AFLTCGSPNSSEYM --ELIWFTRTRSTAVLLYDQEQBQQMTEYRATLATAGL 103	
Qy	69 ITNNLSTVIALRPSDEGTYYCQVLYKEDAFKREHLAETVLSKADFPPPSISDEEPT 128	
Db	104 LDGRATLIRDYRVSDQEGYRC--LFFKDNDDEEE--AAYVLYKVAVGSDFOIS-MTVQE 157	
Qy	129 SNIRRICSTSGGFPEPHLSWLENGEELNAINTVSQDPETELYASSKLDNFMTTNHSF 188	
Db	158 NGEMELECTSSGGWYPPQVQRTGNREMPLSTSESKKHNEEGFLTVAVSMIRDSSIKNM 217	
Qy	189 MCLIK 193	
Db	218 SCIQ 222	
RESULT	15	
ID NCAL_XENLA	STANDARD;	PRT: 1 088 AA.
AC P16170;		PROBABLE.
DT 01-APR-1990 (Rel. 14, Created)	FT DISULFID 323	PROBABLE.
DT 01-APR-1990 (Rel. 14, Last sequence update)	FT DISULFID 379	PROBABLE.
DT 15-JUL-1999 (Rel. 38, Last annotation update)	FT DISULFID 420	PROBABLE.
DEI NEURAL CELL ADHESION MOLECULE 1, LARGE ISOFORM PRECURSOR (N-CAM 180) [CONTAINS: N-CAM 140].	FT DISULFID 473	(POTENTIAL).
GN NCAM1.	FT DISULFID 82	N-LINKED (GLCNAC, . .) (POTENTIAL).
OS Xenopus laevis (African clawed frog).	FT DISULFID 219	N-LINKED (GLCNAC, . .) (POTENTIAL).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	FT DISULFID 310	N-LINKED (GLCNAC, . .) (POTENTIAL).
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;	FT DISULFID 341	N-LINKED (GLCNAC, . .) (POTENTIAL).
OC Xenopidae; Xenopus.	FT DISULFID 417	N-LINKED (GLCNAC, . .) (POTENTIAL).
NCBI_TaxID=83555;	FT DISULFID 443	N-LINKED (GLCNAC, . .) (POTENTIAL).
RN [1] SEQUENCE FROM N.A. MEDLINE=90098871; PubMed=2481269;	FT DISULFID 472	N-LINKED (GLCNAC, . .) (POTENTIAL).
RX	FT VARSPIC 804	MISSING (IN ISOFORM N-CAM 140).
SEQ 1088 AA; 117778 MW; 62738B5B03F3E83 CRC64;	SO 1088	Gaps 9;

Query Match 10.1%; Best Local Similarity 24.0%; Matches 43; Conservative 31; Mismatches 58; Indels 47; Gaps 9;

QY 18 EVATLSCGHNVSVBELAQTRIYQKEKKVNLTMMSGDMNIWPEVKNRPLFDITNNLSIVI 77  
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
Db 130 EDAVILICDVSSISPI---TTWRHKGRDVI----- FKKDVRFLANNYQOI 173  
QY 78 LAIRPSDEGTETYCVLKYEKDAFKREHLAEVTLSVKADPPTPSISDFEI---PTSNIRR- 133  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
Db 174 RGIKKTDEGTYRC---BGRILARGEINYKDIOTVNVP-PTIQARQLRVNATANMAES 227  
QY 134 -IICSTSGGFPPEPHLSWLENGEELNAINTVSODPETELYAVSSKLDFN---MTTNH 186  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
Db 228 VVLSCDADGPDPDETSWLKGEP-----EDGE----EKISFNEQSEMTIH 271

Search completed: April 24, 2002, 15:33:55  
Job time: 191 sec



Database :	SPREMBL_17:*			
1:	sp_archea:*			
2:	sp_bacteria:*			
3:	sp_fungi:*			
4:	sp_human:*			
5:	sp_invertebrate:*			
6:	sp_mammal:*			
7:	sp_minic:*			
8:	sp_organelle:*			
9:	sp_phage:*			
10:	sp_plant:*			
11:	sp_rodent:*			
12:	sp_virus:*			
13:	sp_vertebrate:*			
14:	sp_unclassified:*			

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	1118	97.3	288	6	Q77684	macaca nemorale
2	1100	95.7	288	6	Q28499	macaca mulatta
3	1085	94.4	288	6	Q9DDN6	cercocebus
4	1085	94.4	289	6	Q28347	Q9N2I3
5	764	66.5	230	6	Q9TT70	sus scrofa
6	762.5	66.4	288	6	Q9BE99	Q9T71
7	762.5	66.4	297	6	Q9BE99	sus scrofa
8	761	66.2	229	6	Q9TT71	felis silvestris
9	743	64.7	292	6	Q9GMZ8	Q9GMZ8
10	743	64.7	292	6	Q9GMZ8	Q9GMZ8
11	719	62.6	304	6	Q9IQX1	canis familiaris
12	717.5	62.4	296	6	Q96A05	bos taurus
13	705	61.4	235	6	Q9IQS8	canis familiaris
14	705	61.4	235	6	Q9N0T0	canis familiaris
15	603.5	52.5	321	11	Q35187	rattus norvegicus
16	602	52.4	290	11	Q62680	rattus norvegicus
17	601.5	52.3	321	11	Q62624	rattus norvegicus
18	596	51.9	321	11	Q55202	rattus norvegicus
19	560	48.7	306	11	Q9R1Z9	mus musculus

RESULT 1  
077684 PRELIMINARY; PRT; 288 AA.

ID 077684 ID 077684  
AC AC 077684;  
DT DT .01-NOV-1998 (TREMBLrel. 08, Created)  
DT DT .01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
DT DT .01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE DE B7 PROTEIN.  
GN GN B7.  
OS OS Macaca nemestrina (Pig-tailed macaque).  
OC OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteostomi;  
OC OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC OC Cercopithecinae; Macaca.  
OX OX NCBI\_TaxID:9545;  
RN RN [1]  
RP RP SEQUENCE FROM N.A.  
RA RA Kraus G., Hnatyssyn J.H.;  
RL RL Submitted (JUL-1998) to the EMBL/GenBank/DDJB databases.  
CC CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.  
CC CC DR AF070519; AAC31155.1; -.  
DR DR InterPro; IPR003599; Ig.  
DR DR InterPro; IPR003600; Ig-like.  
DR DR Pfam; PF00047; Ig; 1.  
DR DR SMART; SM00010; Ig; 1.  
SQ SQ SEQUENCE 288 AA; 33131 MW; 76BBC42839E9AB79 CRC64;

Query Match 97.38; Score 1118; DB 6; Length 288;  
Best Local Similarity 97.7%; Pred. No. 3.e-93; 1; Mismatches 210; Conservative 1; Indels 0; Gaps 0;

QY 2 LSHFCSGIVHYTKKEVKAYATLSCGHNVVEAQTRIYQKEKKMVLTMMSGDMN1MPEY 61  
DB 28 LSHFCSGIVTYTKKEVKAYATLSCGHNVVEAQTRIYQKEKKMVLTMMSGDMN1MPEY 87  
QY 62 KNRTIDITNNLSIVIALRPSDEGTIVCVVLYKEDAFKREHLAEFTLSVKADFPPSI 121  
DB 88 KNRTIDITNNLSIVIALRPSDEGTIVCVVLYKEDAFKREHLAEFTLSVKADFPPSI 147

Qy	122	SDFEIPTSNIRLICSTSGGFPPEPHLSWLENGEELNAINTVYSDQDPETELYAVSSKLDFN	181	RESULT	3
Db	148	TDFEIPPSNIRLICSTSGGFPPEPHLSWLENGEELNAINTVYSDQDPETELYAVSSKLDFN	207	Q9BDN6	PRELIMINARY;
Qy	182	MTTNHSFMCILIKYGHLYRNOTFWNTTKQEHFPDN	216	ID Q9BDN6;	PRT;
Db	208	MTTNHSFMCILIKYGHLYRNOTFWNTTPQEHHFPDN	242	AC Q9BDN6;	PRIMER;
RESULT	2			DT 01-JUN-2001 (TREMBLrel.	17, Created)
Q28499		PRELIMINARY;	PRT;	DT 01-JUN-2001 (TREMBLrel.	17, Last sequence update)
ID	Q28499;			DT 01-JUN-2001 (TREMBLrel.	17, Last annotation update)
AC				DE CDS0 PROTEIN	
DT	01-NOV-1996	(TREMBLrel.	01, Created)	GN MNB71.	
DT	01-NOV-1996	(TREMBLrel.	01, Last sequence update)	OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).	
DE	B7 PROTEIN (CD80 PROTEIN PRECURSOR).			OC Fukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OS	GN B7 OR A939.			OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			OC Cercopithecinae; Cercocetus.	
CC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;			NCBI_TAXID=9531;	
CC	Cercopithecinae; Macaca.			RN [1].	
OX	NCBI_TAXID=9544;			RP SEQUENCE FROM N.A.	
RN	[1]			RA Willinger F., Bostick P., Mayne A.E., King C.L., Genain C.P.,	
RN	SEQUENCE FROM N.A.			RA Weiss W.R., Ansari A.A.;	
RX	RX MEDLINE=9603435; PubMed=7561102;			RT Cloning, sequencing and homology analysis of nonhuman primate	
RX	RX PMID=1553946-3954 (1995).			RT Fas/Fas-Ligand and co-stimulatory molecules.;	
RX	RX "Comparative sequence analysis of cytokine genes from human and nonhuman primates".;			RL Immunogenetics 0-0-0(2001);	
RX	RX J. Immunol. 155:3946-3954 (1995).			DR EMBL; AF344839; AAK37535.1;	
RX	RX TISSUE-BLOOD;			DR SEQNE 288 AA; 32917 MW; C6A3F6A3C592972B CRC64;	
Query Match	94.4%	Score 1085;	DB 6;	Length 288;	
Best Local Similarity	95.3%	Pred. No. 3.2e-90;			
Matches	205;	Conservative	4;	Mismatches 6;	Indels 0;
Gaps	0;				
Qy	2	LSHFCSGVIVHTKKEYVATLSGCHNVSYVEELAQTRIYQKEKKAVYLTMMSGDMNITWPEY	61	Q28347;	PRELIMINARY;
Db	28	LSHFCSGVIVHTKKEYVATLSGCHNVSYVEELAQTRIYQKEKKAVYLTMMSGDMNITWPEY	87	AC Q28347;	PRIMER;
Qy	62	KNRIFTDITNNLSIVILALRSPDEGYTCVVKYERDAFKREHLAEVTLVSKADEFPTPSI	121	DT 01-NOV-1996 (TREMBLrel.	01, Created)
Db	88	KNRIFTDITNNLSIVILALRSPDEGYTCVVKYERDAFKREHLAEVTLVSKADEFPTPSI	147	DT 01-NOV-1996 (TREMBLrel.	01, Last sequence update)
Qy	122	SDFEIPTSNIRLICSTGGFPPEPHLSWLENGEELNAINTVYSDQDPETELYAVSSKLDFN	181	DT 01-JUN-2001 (TREMBLrel.	17, Last annotation update)
Db	148	SDFEIPTSNIRLICSTGGFPPEPHLSWLENGEELNAINTVYSDQDPETELYAVSSKLDFN	207	DE B7 PROTEIN (FRAGMENT).	
Qy	182	MTTNHSFMCILIKYGHLYRNOTFWNTTKQEHFPDN	216	GN B7.	
Db	208	MTTNHSFMCILIKYGHLYRNOTFWNTTPQEHHFPDN	242	OS Cercopithecus torquatus (red-crowned mangabey).	
RESULT	4			OC Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
ID	Q28347			OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;	
AC	Q28347;			OC Cercopithecinae; Cercocetus.	
DT	01-NOV-1996 (TREMBLrel.	01, Created)		NCBI_TAXID=9530;	
DT	01-NOV-1996 (TREMBLrel.	01, Last sequence update)		RN [1].	
RT				RP SEQUENCE FROM N.A.	
RT				RC TISSUE-BLOOD;	
RT				RX MEDLINE=9603435; PubMed=7561102;	
RT				RA Willinger F., Brar S.S., Mayne A., Chikkala N., Ansari A.A.;	
RT				"Comparative sequence analysis of cytokine genes from human and nonhuman primates.";	
RL				J. Immunol. 155:3946-3954 (1995).	
- - SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN				- - SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.	
CC SMART; SM00409; IG_1.				DR EMBL; U18833; AAA86700.1;	
CC SMART; SM00410; IG_like; 1.				DR InterPro; IPR00306; Ig_MHC.	
KW SIGNAL.	1	26 POTENTIAL.		DR InterPro; IPR00306; Ig_MHC.	
FT SIGNAL.	288 AA;	33141 MW;	E70BEA4006C7A609 CRC64;	DR Pfam; PF00047; Ig_1.	
SQ				DR SMART; SM00409; IG_1.	
Best Local Similarity	95.7%	Score 1100;	DB 6;	DR SMART; SM00410; IG_like; 1.	
Matches	207;	Conservative	2;	Mismatches 6;	Indels 0;
Gaps	0;			DR SIGNAL.	
Qy	2	LSHFCSGVIVHTKKEYVATLSGCHNVSYVEELAQTRIYQKEKKAVYLTMMSGDMNITWPEY	61	Q28347;	PRELIMINARY;
Db	28	LSHFCSGVIVHTKKEYVATLSGCHNVSYVEELAQTRIYQKEKKAVYLTMMSGDMNITWPEY	87	AC Q28347;	PRIMER;
Qy	62	KNRIFTDITNNLSIVILALRSPDEGYTCVVKYERDAFKREHLAEVTLVSKADEFPTPSI	121	DT 01-NOV-1996 (TREMBLrel.	01, Created)
Db	88	KNRIFTDITNNLSIVILALRSPDEGYTCVVKYERDAFKREHLAEVTLVSKADEFPTPSI	147	DT 01-NOV-1996 (TREMBLrel.	01, Last sequence update)
Qy	122	SDFEIPTSNIRLICSTSGGFPPEPHLSWLENGEELNAINTVYSDQDPETELYAVSSKLDFN	181	DE B7 PROTEIN (FRAGMENT).	
Db	148	TDFEIPPSNIRLICSTSGGFPPEPHLSWLENGEELNAINTVYSDQDPETELYAVSSKLDFN	207	GN B7.	
Qy	182	MTTNHSFMCILIKYGHLYRNOTFWNTTKQEHFPDN	216	OS Cercopithecus torquatus (red-crowned mangabey).	
Db	208	MTTNHSFMCILIKYGHLYRNOTFWNTTPQEHHFPDN	242	OC Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Qy				OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;	
Db				OC Cercopithecinae; Cercocetus.	
Qy				NCBI_TAXID=9530;	
Db				RN [1].	
Qy				RP SEQUENCE FROM N.A.	
Db				RC TISSUE-BLOOD;	
Qy				RX MEDLINE=9603435; PubMed=7561102;	
Db				RA Willinger F., Brar S.S., Mayne A., Chikkala N., Ansari A.A.;	
Qy				"Comparative sequence analysis of cytokine genes from human and nonhuman primates.";	
Db				J. Immunol. 155:3946-3954 (1995).	
Qy				- - SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.	
Db				DR EMBL; U18833; AAA86700.1;	
Qy				DR InterPro; IPR003600; Ig_like.	

DR	InterPro; IPR003006; Ig_MHC.	Qy	121 ISDFEIPTSNIRRICSTGGFPPEHLSWLENGEELAINTVSDPETELYAVSSKLD 180
DR	Pfam; PF00047; Ig_1.	Db	142 ITALGNSPNIKRTRCSSTGGFPPEHLSWLENGEELAINTVSDPETELYAVSSKLD 201
* FT	SMART; SM00410; Ig-like; 2.	Qy	181 NMNTNHSEMCLIKYGHLYRVNOTENWNTTK 209
NON_TER	289	Db	202 NVTGNHSEMCLVKYGLTVSQTFNWQCK 230
SEQUENCE	289 AA;	33030 MW;	5ED6A3F6A3C59297 CRC64;
Query Match	94.4%; Score 1085; DB 6; Length 289;	RESULT 6	
Best Local Similarity	95.3%; Pred. No. 3.2e-90;	Q9TT70 PRELIMINARY;	PRT; 288 AA.
Matches 205; Conservative 4; Mismatches 6; Indels 0; Gaps 0;	ID Q9TT70	AC 01-MAY-2000 (TREMBLrel. 13, Created)	DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
Qy 2 LSHRCGSVTHVTKEVKEYATLSCCHNVSVEELAQTRIYQKEKKMVLTTGGDMNIWPEY 61	RA Fodor W.L., Mueller J.P., Matis L.A., Rother R.P.;	DT 01-MAY-2000 (TREMBLrel. 17, Last annotation update)	DE CD80 PROTEIN PRECURSOR (FRAGMENT).
Db 28 LSHRCGSVTHVTKEVKEYATLSCCHNVSVEELAQTRIYQKEKKMVLTTGGDMNIWPEY 87	RA Faas S.J., Giannoni M.A., Micklem A., Kiesecker C.L., Reed D.J., Wu D., NCBI_TaxID=9823;	RN [1]	
Qy 62 KNRTIFDITNNLSTIVLALRPSDEGTYYCVLVKEYDAFKREHIAEVTLVSKVADEPPTSI 121	RA "Primary Structure and Functional Characterization of a Soluble, Alternately Spliced Form of B7-1.";	RP SEQUENCE FROM N.A.	
Db 88 KNRTIFDITNNLSTIVLALRPSDEGTYYCVLVKEYDAFKREHIAEVTLVSKVADEPPTSI 147	RL Submitted (Nov 1999) to the EMBL/GenBank/DBJ databases.	RA "Primary Structure and Functional Characterization of a Soluble, Alternately Spliced Form of B7-1.";	
Qy 122 SDFFEIPTSNIRRICSTGGFPPEHLSWLENGEELAINTVSDPETELYAVSSKLD 181	CC -I SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN	RA "Primary Structure and Functional Characterization of a Soluble, Alternately Spliced Form of B7-1.";	
Db 148 TDFEIPPSNIRRICSTGGFPPEHLSWLENGEELAINTVSDPETELYAVSSKLD 207	CC DOMAIN; AF203443; AAF22750.1; - .	RA "Primary Structure and Functional Characterization of a Soluble, Alternately Spliced Form of B7-1.";	
Qy 182 MTNTNHSEMCLIKYGHLYRVNOTENWNTTKOEHFPDN 216	DR Interpro; IPR003599; Ig.	RA "Primary Structure and Functional Characterization of a Soluble, Alternately Spliced Form of B7-1.";	
Db 208 MTNTNHSEMCLIKYGHLYRVNOTENWNTTKOEHFPDN 242	DR Interpro; IPR003600; Ig-like.	RA "Primary Structure and Functional Characterization of a Soluble, Alternately Spliced Form of B7-1.";	
Qy 183 Q9N213 PRELIMINARY; PRT; 230 AA.	DR Interpro; IPR003006; Ig_MHC.	RA "Primary Structure and Functional Characterization of a Soluble, Alternately Spliced Form of B7-1.";	
DR	Q9N213 ID 01-OCT-2000 (TREMBLrel. 15, Created)	CC SMART; SM00409; Ig. 1.	
AC	01-OCT-2000 (TREMBLrel. 15, Last sequence update)	DR SMART; SM00410; Ig_1-like; 1.	
DR	01-JUN-2001 (TREMBLrel. 17, Last annotation update)	KW SIGNAL. 66.4%; Score 762.5; DB 6; Length 288;	
CC	DE CD80 PROTEIN PRECURSOR.	FT SIGNAL. 66.5%; Pred. No. 4.4e-61; Best Local Similarity 66.5%; Mismatches 42; Indels 1; Gaps 1;	
GN	CD80/B7.	FT CHAIN 1 29	CD80 PROTEIN
OS	Sus scrofa (Pig).	FT NON-TER 30 >288	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suiна; Suidae; Sus .	SQ SEQUENCE 288 AA; 32510 MW; 67E31D0FD845D1CB CRC64;	
NCBI_TaxID=9823;		Query Match Score 762.5; DB 6; Length 288;	
OX [1]		Best Local Similarity 66.5%; Pred. No. 4.4e-61; Mismatches 42; Indels 1; Gaps 1;	
RP	SEQUENCE FROM N.A.	Matches 141; Conservative 28; Mismatches 42;	
Qy 184 Q9N214 PRELIMINARY; PRT; 230 AA.	CC -I SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN	Qy 1 GLSHFCGSVHYTKKEYAVTLCGHNVSVEELAQTRIYQKEKKMVLTTGGDMNIWPE 60	
DR	Wada M., Amae S., Hoshi M., Nio M., Ohi R.;	DR 22 GLDFDCCGIVQVTKTKEAVLSDNISTEELTRVYWORDNEAVLNSGVKVWPK 81	
DR	"Porcine CD80(B-7) mRNA, partial cds."	Qy 61 YKNRTIFDITNNLSTIVLALRPSDEGTYYCVLVKEYDAFKREHIAEVTLVSKVADEPPTPS 120	
DR	Submitted (APR-99) to the EMBL/GenBank/DBJ databases.	CC -I SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN	
CC	-I SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN	DR 82 YENRTFDTVNNUCIVTLLALRSLDNGTYTCVYQKREGSYYKUHLTSVKLAVKADFPVPS 141	
DR	EMBL; AB026121; BAA90700.2; - .	DR Interpro; IPR003599; Ig.	
DR	Interpro; IPR003599; Ig.	DR Interpro; IPR003600; Ig-like.	
DR	Interpro; IPR003006; Ig_MHC.	DR Interpro; IPR003006; Ig_MHC.	
DR	Pfam; PF00047; Ig_2.	DR SMART; SM00409; Ig. 1.	
DR	SMART; SM00409; Ig. 1.	DR SMART; SM00410; Ig_1-like; 1.	
KW	Signal. 1 29 POTENTIAL.	KW SIGNAL. 66.5%; Score 764; DB 6; Length 230;	
FT	CHAIN 30 230 MW; POTENTIAL.	FT SIGNAL. 66.5%; Pred. No. 2.4e-61; Best Local Similarity 67.0%; Mismatches 43; Indels 0; Gaps 0;	
SEQ	230 AA; EB63AD172663C4A4 CRC64;	FT CHAIN 1 29 POTENTIAL.	
Qy 1 GLSHFCGSVHYTKKEYAVTLCGHNVSVEELAQTRIYQKEKKMVLTTGGDMNIWPE 60	Qy 181 NMNTNHSEMCLIKYGHLYRVNOTENWNTTK 211	Qy 1 NMNTNHSEMCLIKYGHLYRVNOTENWNTTK 211	
Db 22 GLDFDCCGIVQVTKTKEAVLSDNISTEELTRVYWORDNEAVLNSGVKVWPK 81	Db 142 ITALGNSPNIKRTRCSSTGGFPPEHLSWLENGEELAINTVSDPETELYAVSSKLD 201	Db 202 NVTGNHSEMCLVKYGLTVSQTFNWQSAKRE 233	
Qy 61 YKNRTIFDITNNLSTIVLALRPSDEGTYYCVLVKEYDAFKREHIAEVTLVSKVADEPPTPS 120	Qy 1 NMNTNHSEMCLIKYGHLYRVNOTENWNTTK 211	Qy 1 NMNTNHSEMCLIKYGHLYRVNOTENWNTTK 211	
Db 82 YENRTFDTVNNUCIVTLLALRSLDNGTYTCVYQKREGSYYKUHLTSVKLAVKADFPVPS 141	Db 202 NVTGNHSEMCLVKYGLTVSQTFNWQSAKRE 233	Db 202 NVTGNHSEMCLVKYGLTVSQTFNWQSAKRE 233	
Query Match 66.5%; Score 764; DB 6; Length 230;	Result 7	Q9EE99 PRELIMINARY; PRT; 297 AA.	
Best Local Similarity 67.0%; Mismatches 43; Indels 0; Gaps 0;	ID Q9EE99	AC Q9EE99	
Matches 140; Conservative 26; Mismatches 43; Indels 0; Gaps 0;	AC Q9EE99	DT 01-JUN-2001 (TREMBLrel. 17, Created)	
Qy 1 GLSHFCGSVHYTKKEYAVTLCGHNVSVEELAQTRIYQKEKKMVLTTGGDMNIWPE 60	DB DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)		
Db 22 GLDFDCCGIVQVTKTKEAVLSDNISTEELTRVYWORDNEAVLNSGVKVWPK 81			
Qy 61 YKNRTIFDITNNLSTIVLALRPSDEGTYYCVLVKEYDAFKREHIAEVTLVSKVADEPPTPS 120			
Db 82 YENRTFDTVNNUCIVTLLALRSLDNGTYTCVYQKREGSYYKUHLTSVKLAVKADFPVPS 141			

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)	DR EMBL; AB038153; BAA90764_1; -.
DE CD80 PROTEIN PRECURSOR.	DR InterPro; IPR003599; Ig_like.
GN CD80/B7-1.	DR InterPro; IPR003600; Ig_like.
OS Sus scrofa (Pig).	DR InterPro; IPR003006; Ig_MHC.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	PFam; PF00047; ig_2.
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.	SMART; SM00409; Ig_1.
OX NCBI_TaxID:9823;	SMART; SM00410; Ig_like; 1.
RN [1]	KW Signal.
RP SEQUENCE FROM N.A.	FT SIGNAL 1 29
RC STRAIN=LANDRACE; TISSUE=ILEUM MUCOSA;	FT CHAIN 1 30 229 AA; CD80 PROTEIN.
RA Wada M., Amae S., Sano N., Ishii T., Hoshi M., Nio M.,	SEQUENCE 229 AA; C3AD172663CA4ED CRC64;
RA Hayashi Y., Ohi R.,	
RT "cloning and sequencing of cDNAs for porcine B7-1 (CD80) and soluble isoforms";	
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.	Query Match 66.2%; Score 761; DB 6;
DR EMBL; AB049760; BAB40952.1; -.	Best Local Similarity 67.8%; Pred. No. 4.5e-60; Mismatches 40; Indels 0; Gaps 0;
KW SIGNAL.	Matches 139; Conservative 26; Mismatches 40; Indels 0; Gaps 0;
FT SIGNAL 1 29 POTENTIAL.	QY 1 GLSHFCSGVIVHTKEYKEVATLSCGHNVSVEELAQTRIYQKERRQMVLTMMSGDMNWIPE 60
SQ SEQUENCE 297 AA; 33438 MW; 23109711EA63EF23 CRC64;	Db 22 GLDFCSCIVQTQTKTVAIVSCDYNISTEELTRVRYWORDNEVMYAVMSCKVKWPK 81
Query Match 66.4%; Score 762.5; DB 6; Length 297;	Query Match 66.2%; Score 761; DB 6;
Best Local Similarity 66.5%; Pred. No. 4.5e-61; Mismatches 42; Indels 1; Gaps 1;	Best Local Similarity 67.8%; Pred. No. 4.5e-60; Mismatches 40; Indels 0; Gaps 0;
Matches 141; Conservative 28; Mismatches 42; Indels 1; Gaps 1;	Matches 139; Conservative 26; Mismatches 40; Indels 0; Gaps 0;
QY 1 GLSHFCSGVIVHTKEYKEVATLSCGHNVSVEELAQTRIYQKERRQMVLTMMSGDMNWIPE 60	QY 1 YKRTTIFTINNLISIVIALRPSDEGYECVVLKYERDAFKREHLAETVLSVKADEFPTPS 120
Db 22 GLDFCSCIVQTQTKTVAIVSCDYNISTEELTRVRYWORDNEVMYAVMSCKVKWPK 81	Db 82 YENRTFIVNNICIVILALRSNDGTYTCVQVKRERGSYKLEHTSVKLMYKADFPVPS 141
QY 61 YKRTTIFTINNLISIVIALRPSDEGYECVVLKYERDAFKREHLAETVLSVKADEFPTPS 120	QY 121 ISDFEPTSNTRIICSTGGPPPEPHLSWLENGEELNAINNTVSQDPETELYAVSSKLF 180
Db 82 YENRTFIVNNICIVILALRSNDGTYTCVQVKRERGSYKLEHTSVKLMYKADFPVPS 141	Db 142 ITALGNNSPNKIRCTSGGPPPEPHLSWLENGEELNAINNTVSQDPETELYAVSSKLF 201
Qy 121 ISDFEPTSNTRIICSTGGPPPEPHLSWLENGEELNAINNTVSQDPETELYAVSSKLF 180	RESULT 9
Db 142 ITALGNNSPNKIRCTSGGPPPEPHLSWLENGEELNAINNTVSQDPETELYAVSSKLF 201	002758 ID 002758 PRELIMINARY; PRT; 292 AA.
Qy 181 NMTTNHSFMCILKYGHLRVNOTFW-NTTKOF	AC 002758 ID 002758 PRELIMINARY; PRT; 292 AA.
Db 202 NVTGNHSFMCILKYGGLTVSONFNOKSAKRE 233	DT 01-JUL-1997 (TREMBLrel. 04, Created)
RESULT 8	DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
ID Q9TT71 PRELIMINARY; PRT; 229 AA.	DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
AC Q9TT71 PRELIMINARY; PRT; 229 AA.	CC - SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DT 01-MAY-2000 (TREMBLrel. 13, Created)	CC DOMAIN
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)	DR EMBL; U57755; AAB53575_1; -.
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)	DR InterPro; IPR003600; Ig_like.
DE CD80 PROTEIN PRECURSOR.	DR InterPro; IPR003006; Ig_MHC.
GN CD80/B7-1.	DR Pfam; PF00047; ig_1.
OS Sus scrofa (Pig).	DR SMART; SM00410; Ig_like; 2.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	DR SEQUENCE 292 AA; 33482 MW; 6F117E7852B7950F CRC64;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.	Query Match 64.7%; Score 743; DB 6; Length 292;
OX NCBI_TaxID:9823;	Best Local Similarity 63.3%; Pred. No. 2.6e-59; Mismatches 33; Indels 44; Gaps 1;
RN [2]	Matches 136; Conservative 33; Mismatches 44; Indels 2; Gaps 1;
RP SEQUENCE FROM N.A.	Qy 2 LSHFCSGVIVHTKEYKEVATLSCGHNVSVEELAQTRIYQKERRQMVLTMMSGDMNWIPEY 61
RA Fodor W.L., Mueller J.P., Matis L.A., Rother R.P.;	Db 28 LFYFCSCIGI-QVNKTVEAVLSCDYNISTKELTERIYWORDNEVMYAVMSGKVQWPX 87
RT "Primary Structure and Functional Characterization of a Soluble, Alternatively Spliced Form of B7-1";	Qy 62 KNR1FDITNNLISIVIALRPSDEGYECVVLKYERDAFKREHLAETVLSVKADEFPTPSI 121
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.	Db 88 KNR1FDITNNLISIVIALRPSDEGYECVVLKYERDAFKREHLAETVLSVKADEFPTPSI 147
RN [2]	CC DOMAIN; AF203442; AAF22749.1; -.
RC TISSUE=SPIEEN;	DR EMBL; AF203442; AAF22749.1; -.
*RA Wada M., Amae S., Hoshi M., Nio M., Ishii T., Sano N., Sasaki H., RA R.;	
RT "Splicing Isoform of Porcine CD80.";	
RT "Primary Structure and Functional Characterization of a Soluble, Alternatively Spliced Form of B7-1";	
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.	
CC DOMAIN; TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX	
DR EMBL; AF203442; AAF22749.1; -.	

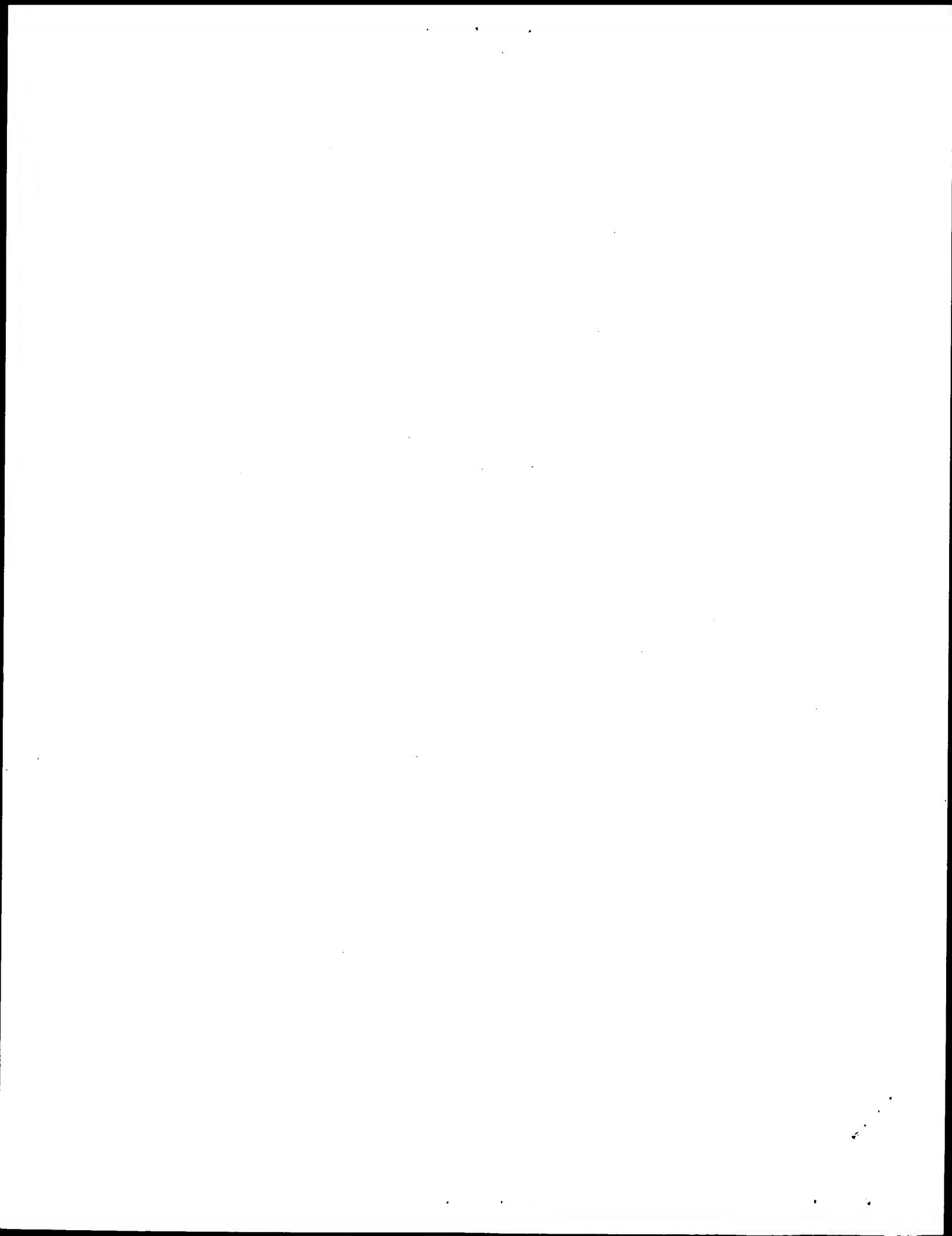


DR	SMART; SM00409; IG_1.	62.4%; Score 717.5; DB 6; Length 296;	QY	62 KNRIFDITNNLSTIVLALRPSDEGYECVVLKYEKDAFKREHLAETLSVKADPPTPSI 121	Db	28 LFYFCSGIQLQVNKTVKVEAVLSCDYNISTTELMKVRYMDDEVVLAVTSGOTKWKSY 87
KW	SIGNAL.	POTENTIAL.	QY	61.5%; Pred. No. 5.4e-56;	Db	62 ENRTFADFTNNLSTIVLALRSDNGKYTCVQTKRSYKHMVMLVRADFPVPSI 147
FT	NON_TER	296	296	296	Db	63 TDLGNSPDIDKRMCSSTCGFPKPHLSWNEEELNANTVSQDPDTELYTISSELDFN 207
SQ	SEQUENCE	296 AA;	33618 MW;	7ADB11FB5F532EFD5 CRC64;	Db	64 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETELYAVSSKLDFN 181
Query Match	Best Local Similarity 62.4%; Score 717.5; DB 6; Length 296;	Potential.	QY	65 :    :    :    :    :    :    :    :    :    :    :    :    :    :    :	Db	65 ENRTFADFTNNLSTIVLALRSDNGKYTCVQTKRSYKHMVMLVRADFPVPSI 147
Best Local Similarity 63.2%; Pred. No. 5.3e-57; Mismatches 28; Indels 3; Gaps 2;	Matches 134; Conservative 28; Mismatches 47; Indels 3; Gaps 2;	Db	66 MTNHSFVCLVKYGDLTYSQIFNWQCK 209			
QY	1 GLSHFCGCVI-HVTKKEYVATLSCGHNVSEELAQTRIYQWERKMKVLTMMMSGDMNTW 58	Db	67 MTNHSFVCLVKYGDLTYSQIFNWQCK 235			
Db	27 GLYFCGSGITPKSVPKRVETPLSCLDVNTSTEELTSRLYQWORDSKMVLAILGKVQWV 86	Db	68 ITSNHSFVCLVKYGDLTYSQIFNWQCK 235			
QY	59 PEYKNRFTFDITNNLSTIVLALRPSDEGYECVVLKYE-KDAFKREHLAETLSVKADFP 117	RESULT 14	Q9NOTO	PRELIMINARY;	Db	69 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETELYAVSSKLDFN 181
Db	87 PEYKNRFTTDMMENPRIVTLALRSLDSGTYTQKPDJKAYKLEHTLSVRLMIRADFP 146	Q9NOTO	ID	70 PRELIMINARY;	Db	71 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETELYAVSSKLDFN 181
QY	118 TPS-TSDFEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETELYAVSSK 177	AC	AC	72 PRELIMINARY;	Db	73 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETELYAVSSKLDFN 181
Db	147 VPIINDLGNPSNPINRLLCSTSGGFPPEHLSWLENGEELNAINTVSDQPETKLIMISSE 206	DT	DT	74 PRELIMINARY;	Db	75 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETLYAVSSKLDFN 181
QY	178 LEENMTNHSFMCLIKIGHLRVQTFNWNTTK 209	DT	DT	76 PRELIMINARY;	Db	77 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETLYAVSSKLDFN 181
Db	207 LEENMTNHSFVCLVKYGDLTYSQTFYWQESK 238	DT	DT	78 PRELIMINARY;	Db	79 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETLYAVSSKLDFN 181
QY	208 ITSNHSFVCLVKYGDLTYSQIFNWQCK 235	DT	DT	80 PRELIMINARY;	Db	81 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETLYAVSSKLDFN 181
RESULT 13	Q9TQS8	PRELIMINARY;	PRY;	82 PRELIMINARY;	Db	83 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETLYAVSSKLDFN 181
ID	Q9TQS8	PRY;	PRY;	84 PRELIMINARY;	Db	85 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETLYAVSSKLDFN 181
AC	Q9TQS8	PRY;	PRY;	86 PRELIMINARY;	Db	87 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETLYAVSSKLDFN 181
DT	01-MAY-2000 (TREMBLrel. 13 Created)	PRY;	PRY;	88 PRELIMINARY;	Db	89 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETLYAVSSKLDFN 181
DT	01-MAY-2000 (TREMBLrel. 13 Last sequence update)	PRY;	PRY;	90 PRELIMINARY;	Db	91 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETLYAVSSKLDFN 181
DT	01-JUN-2001 (TREMBLrel. 17 Last annotation update)	PRY;	PRY;	92 PRELIMINARY;	Db	93 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETLYAVSSKLDFN 181
DE	SECRETED B7-1 PROTEIN PRECURSOR.	PRY;	PRY;	94 PRELIMINARY;	Db	95 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETLYAVSSKLDFN 181
GN	CD80.	PRY;	PRY;	96 PRELIMINARY;	Db	97 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETLYAVSSKLDFN 181
OS	Canis familiaris (Dog).	PRY;	PRY;	98 PRELIMINARY;	Db	99 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETLYAVSSKLDFN 181
OC	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	PRY;	PRY;	100 PRELIMINARY;	Db	101 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETLYAVSSKLDFN 181
OC	Mammalia; Eutheria; Carnivora; Pissipedia; Canidae; Canis.	PRY;	PRY;	102 PRELIMINARY;	Db	103 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETLYAVSSKLDFN 181
NCBI_TaxID	9615;	PRY;	PRY;	104 PRELIMINARY;	Db	105 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETLYAVSSKLDFN 181
RN	[1]	PRY;	PRY;	106 PRELIMINARY;	Db	107 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETLYAVSSKLDFN 181
RX	SEQUENCE FROM N.A. MEDLINE=20093996; PubMed=10630300;	PRY;	PRY;	108 PRELIMINARY;	Db	109 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETLYAVSSKLDFN 181
RT	"New Forms of Dog CD80 and CD86 Transcripts that Encode Secreted B7 Molecules." Yang S., Sim G.-K.; RT	PRY;	PRY;	110 PRELIMINARY;	Db	111 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETLYAVSSKLDFN 181
CC	Immunogenetics 50:349-353(1999). -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.	PRY;	PRY;	112 PRELIMINARY;	Db	113 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETLYAVSSKLDFN 181
CC	EMBL; AF106825; AAF17296.1; DR	PRY;	PRY;	114 PRELIMINARY;	Db	115 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETLYAVSSKLDFN 181
CC	EMBL; AF106831; AAF17294.1; DR	PRY;	PRY;	116 PRELIMINARY;	Db	117 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETLYAVSSKLDFN 181
CC	EMBL; AF106829; AAF17294.1; JOINED. DR	PRY;	PRY;	118 PRELIMINARY;	Db	119 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETLYAVSSKLDFN 181
CC	EMBL; AF106830; AAF17294.1; JOINED. DR	PRY;	PRY;	120 PRELIMINARY;	Db	121 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETLYAVSSKLDFN 181
CC	EMBL; AF106830; AAF17294.1; JOINED. DR	PRY;	PRY;	122 PRELIMINARY;	Db	123 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETLYAVSSKLDFN 181
CC	InterPro; IPR003599; Ig_1. InterPro; IPR003600; Ig_1-like. Pfam; PF000047; ig_1. SMART; SM00409; Ig_1. Signal; SR00410; Ig_like_1.	PRY;	PRY;	124 PRELIMINARY;	Db	125 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETLYAVSSKLDFN 181
CC	Signal; SR00410; Ig_like_1. SIGNAL CHAIN 34 MW; SECRETED B7-1 PROTEIN.	PRY;	PRY;	126 PRELIMINARY;	Db	127 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETLYAVSSKLDFN 181
CC	SEQUENCE 235 AA; 26917 MW; CC08CAA676BCB40A CRC64;	PRY;	PRY;	128 PRELIMINARY;	Db	129 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETLYAVSSKLDFN 181
Query Match	Best Local Similarity 61.4%; Score 705; DB 6; Length 235;	PRY;	PRY;	130 PRELIMINARY;	Db	131 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETLYAVSSKLDFN 181
Best Local Similarity 61.5%; Pred. No. 5.4e-56; Matches \ 18; Conservative 33; Mismatches 47; Indels 0; Gaps 0;	PRY;	PRY;	132 PRELIMINARY;	Db	133 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETLYAVSSKLDFN 181	
QY	2 LSFHFCGCVI-HVTKKEYVATLSCGHNVSEELAQTRIYQWERKMKVLTMMMSGDMNTW 61	PRY;	PRY;	134 PRELIMINARY;	Db	135 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETLYAVSSKLDFN 181
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QY	2 LSFHFCGCVI-HVTKKEYVATLSCGHNVSEELAQTRIYQWERKMKVLTMMMSGDMNTW 61	PRY;	PRY;	138 PRELIMINARY;	Db	139 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETLYAVSSKLDFN 181
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QY	2 LSFHFCGCVI-HVTKKEYVATLSCGHNVSEELAQTRIYQWERKMKVLTMMMSGDMNTW 61	PRY;	PRY;	144 PRELIMINARY;	Db	145 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETLYAVSSKLDFN 181
QY	2 LSFHFCGCVI-HVTKKEYVATLSCGHNVSEELAQTRIYQWERKMKVLTMMMSGDMNTW 61	PRY;	PRY;	146 PRELIMINARY;	Db	147 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETLYAVSSKLDFN 181
QY	2 LSFHFCGCVI-HVTKKEYVATLSCGHNVSEELAQTRIYQWERKMKVLTMMMSGDMNTW 61	PRY;	PRY;	148 PRELIMINARY;	Db	149 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETLYAVSSKLDFN 181
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QY	2 LSFHFCGCVI-HVTKKEYVATLSCGHNVSEELAQTRIYQWERKMKVLTMMMSGDMNTW 61	PRY;	PRY;	158 PRELIMINARY;	Db	159 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETLYAVSSKLDFN 181
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QY	2 LSFHFCGCVI-HVTKKEYVATLSCGHNVSEELAQTRIYQWERKMKVLTMMMSGDMNTW 61	PRY;	PRY;	166 PRELIMINARY;	Db	167 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETLYAVSSKLDFN 181
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QY	2 LSFHFCGCVI-HVTKKEYVATLSCGHNVSEELAQTRIYQWERKMKVLTMMMSGDMNTW 61	PRY;	PRY;	172 PRELIMINARY;	Db	173 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETLYAVSSKLDFN 181
QY	2 LSFHFCGCVI-HVTKKEYVATLSCGHNVSEELAQTRIYQWERKMKVLTMMMSGDMNTW 61	PRY;	PRY;	174 PRELIMINARY;	Db	175 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETLYAVSSKLDFN 181
QY	2 LSFHFCGCVI-HVTKKEYVATLSCGHNVSEELAQTRIYQWERKMKVLTMMMSGDMNTW 61	PRY;	PRY;	176 PRELIMINARY;	Db	177 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETLYAVSSKLDFN 181
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QY	2 LSFHFCGCVI-HVTKKEYVATLSCGHNVSEELAQTRIYQWERKMKVLTMMMSGDMNTW 61	PRY;	PRY;	180 PRELIMINARY;	Db	181 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETLYAVSSKLDFN 181
QY	2 LSFHFCGCVI-HVTKKEYVATLSCGHNVSEELAQTRIYQWERKMKVLTMMMSGDMNTW 61	PRY;	PRY;	182 PRELIMINARY;	Db	183 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETLYAVSSKLDFN 181
QY	2 LSFHFCGCVI-HVTKKEYVATLSCGHNVSEELAQTRIYQWERKMKVLTMMMSGDMNTW 61	PRY;	PRY;	184 PRELIMINARY;	Db	185 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETLYAVSSKLDFN 181
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QY	2 LSFHFCGCVI-HVTKKEYVATLSCGHNVSEELAQTRIYQWERKMKVLTMMMSGDMNTW 61	PRY;	PRY;	188 PRELIMINARY;	Db	189 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETLYAVSSKLDFN 181
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QY	2 LSFHFCGCVI-HVTKKEYVATLSCGHNVSEELAQTRIYQWERKMKVLTMMMSGDMNTW 61	PRY;	PRY;	194 PRELIMINARY;	Db	195 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETLYAVSSKLDFN 181
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QY	2 LSFHFCGCVI-HVTKKEYVATLSCGHNVSEELAQTRIYQWERKMKVLTMMMSGDMNTW 61	PRY;	PRY;	208 PRELIMINARY;	Db	209 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETLYAVSSKLDFN 181
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QY	2 LSFHFCGCVI-HVTKKEYVATLSCGHNVSEELAQTRIYQWERKMKVLTMMMSGDMNTW 61	PRY;	PRY;	232 PRELIMINARY;	Db	233 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETLYAVSSKLDFN 181
QY	2 LSFHFCGCVI-HVTKKEYVATLSCGHNVSEELAQTRIYQWERKMKVLTMMMSGDMNTW 61	PRY;	PRY;	234 PRELIMINARY;	Db	235 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETLYAVSSKLDFN 181
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QY	2 LSFHFCGCVI-HVTKKEYVATLSCGHNVSEELAQTRIYQWERKMKVLTMMMSGDMNTW 61	PRY;	PRY;	244 PRELIMINARY;	Db	245 SDPEIPTSNIRRILCSTSGGFPPEHLSWLENGEELNAINTVSDQPETLYAVSSKLDFN 181
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QY	2 LSFHFCGCVI					

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DB B7.1.  
 GN Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OC NCBI\_TaxID:10116;  
 RN [1]  
 RP  
 SEQUENCE FROM N. A.  
 RC STRAIN=FISCHER;  
 RA Widegren B., Visse E., Sjogren H.O.; Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
 RL -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
 CC DOMAIN  
 EMBL; AF010465; AAB66351..1.; ~.  
 DR InterPro; IPR00599; Ig.  
 DR InterPro; IPR005600; Ig\_like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; Ig\_2.  
 DR SMART; SM00409; Ig\_1.  
 DR SMART; SM00410; Ig\_like\_1.  
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 SQ 321 AA; 36351 MW; 071CC007FBBD1E80 CRC64;  
 SEQUENCE

Query Match 52.5%; Score 603.5; DB 11; Length 321;  
 Best Local Similarity 54.9%; Pred. No. 1..2e-45;  
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 Db 31 GFQISSGIVGQVSKSYREKALLSDIKFCSEEQSIRIYQKHDKMVLSTISGYPEVWP 90  
 Qy 60 EYKNPTIEDTNNLISIYVLAIRPSDDETYECVVKYEKDAFKREHTLAEVTLVKADEPTP 119  
 Db 91 EYKNRTYDIANNYSEFLGLLSDRTYTCVQRGESESVVKHHTTVELSVRADEPPTP 150  
 Qy 120 SISDFEPLTSNIRRITCSTSQQFPEPHLSWLENGEELNAINTVSQDPETELYAYSSKLD 179  
 Db 151 NITESGMPSPADIKRITCFASGGFPKPRUSWLENGEREELNTTISODPESELYTISQLD 210  
 Qy 180 FNNTTNNHSFMCUJKYGLRVRNFTNW 205  
 Db 211 FNTTYDHIFDCPIEYGAHVSONTW 236

Search completed: April 24, 2002, 15:33:37  
 Job time: 193 sec



GanCore version 4.5  
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## OM protein - protein search, using sw model

Run on: April 24, 2002, 15:26:09 ; Search time 23.25 Seconds

(without alignments)  
(88.165 Million cell updates/sec  
Title: US-09-454-651B-23  
Sequence: 1 GLSHFCSSGYTHVKVEVA.....LRYNQTFNNNTKQEHFPDN 216

Scoring table: BLOSUM62

Gapop 10.0 , Gapext. 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 10%

Maximum Match 10%  
Listing first 45 summaries

Database : A\_Geneseq\_1101:\*

1: /SIDSB8/gcldata/geneseq/geneseqp/AA1980.DAT:\*

2: /SIDSB8/gcldata/geneseq/geneseqp/AA1981.DAT:\*

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RESULT 1

AAR67989

ID AAR67989 standard; protein; 288 AA.

XX

AC AAR67989;

XX

21-AUG-1995 (first entry)

DT

XX

Human B lymphocyte antigen B7-1 (hB7-1).

DE

XX

B lymphocyte antigen B7-1; B cell activation antigen; CD28;

KW

KW

Ligand; T cell surface antigen; transmembrane protein.

XX

OS Homo sapiens.

XX

FH Key

FT Protein

FT

FT	Misc-difference	/label= see above	XX	DT 08-APR-1998 (first entry)
FT	Misc-difference	211..213	XX	XX
FT	Misc-difference	/label= see above	DE B7-1.	DE
FT	Misc-difference	226..228	XX	KW Screening; inhibitor; enhancer; binding; CD28; B7-1.
FT	Misc-difference	/label= see above	XX	XX
FT	Misc-difference	232..234	OS	Homo sapiens.
Domain	Domain	35..138	XX	
FT	Domain	/label= Ig V-set domain	PN	EP795554-A2.
FT	Domain	139..236	XX	
XX	/label= Ig C-set domain	PD 17-SEP-1997.	XX	
PN	W09503408-A.	PF 04-MAR-1997;	XX	PF 97EP-0301438.
XX	PD 02-FEB-1995.	PR 02-OCT-1996;	XX	PR 96JP-0362085.
XX	PF 26-JUL-1994;	PR 05-MAR-1996;	XX	PR 96JP-0047795.
XX	94WO-US08423.	PA (TAKE ) TAKEDA CHEM IND LTD.	XX	
PR	26-JUL-1993;	PT New xanthene derivatives useful as immunomodulators - e.g. methyl 2-(carboxymethyl)xanthine-5,7-dichloro-3,8-dihydroxy-6-	XX	
PR	19-AUG-1993;	PT 2-hydroxy-9H-xanthene-1-carboxylate.	XX	
PR	03-NOV-1993;	PT methyl-1-9-oxo-9H-xanthene-1-carboxylate.	XX	
XX	93US-010933.	DR WPI; 1997-450803/42.	DR	
XX	93US-014773.	N-PSDB; AAW96358.	N-PSDB	
PA	(DAND ) DANA FARBER CANCER INST INC.	PS Disclosure; Fig 4; 117pp; English.	PS	
PA	(REPK ) REPLICEN CORP.	XX	XX	
XX	PA (REPK ) REPLICEN CORP.	CC The present sequence was used in the development of a novel method	CC	
PI	Freeman GJ,	PI Hattori M, Hida T, Kurokawa T, Nakanishi A;	PI	
XX	Gray GS,	XX	XX	
XX	Greenfield E,	XX	XX	
XX	Nadler LM;	XX	XX	
DR	WPI; 1995-075236/10.	XX	XX	
DR	N-PSDB; AAW81370.	PS Sequence 288 AA;	PS	
XX	XX	Query Match 100.0%; Score 1149; DB 18; Length 288;	QY	61 YKNRTFIDITNNLIVIALRPSDEGTYECVLYKEKDAFKREHLAEVTLSVKADFPPTPS 120
PT	Nucleic acids encoding CTLA4/CD28 counter receptor, B7-2 - useful	Best Local Similarity 100.0%; Pred. No. 2e-103; Mismatches 0; Indels 0; Gaps 0;	Db	87 yknrtfidiitnnliviialrpsdegtyscvlykekdafkrehlaevtlsvkadfpptps 146
PT	for enhancing or suppressing T-cell mediated immune responses	Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	QY	121 ISDFEFLPTSNIRRITICSTSGGFPEPHLSWLENGEELNATNTVSODPETLYAVSSKLD 180
XX	Disclosure; pages 111-113; 175pp; English.	CC to B7-1.	Db	147 isdfefiptsnirriticsstsgfpephlswlengeelnaainttvsqdpetelyavsskldf 206
CC	Q81371 is in pcDM8 vector. It is derived from lymphoid B cells, cell line Raji, clone no. 13. Its position in the genome is	CC	QY 1 GLSHFCSGVTHVTKEYVALSCHGNVSVELAQTRIYQKEKKMVLTMMSGDMNTIWE 60	
CC	chromosome/segment 3. It was published by Freeman, F.J. et al., J. of Immunology, 143: 8; 2714-2722, 15th October 1989. It can be found in Genbank at Accession No. M27533. The encoded protein, R67989, binds both human CTLA4 and human CD8. It is related to human hb7-2 (see Q81351) and murine hb7 (see Q81372).	CC	Db 27 gishfcsgvihvtkeyvalschgnvsveelaqtriyqkekkmvltnmsgdmntiwe 86	
PS	Sequence 288 AA;	XX	QY 62 YKNRTFIDITNNLIVIALRPSDEGTYECVLYKEKDAFKREHLAEVTLSVKADFPPTPS 146	
XX	Q81371 is in pcDM8 vector. It is derived from lymphoid B cells, cell line Raji, clone no. 13. Its position in the genome is	CC	Db 87 yknrtfidiitnnliviialrpsdegtyscvlykekdafkrehlaevtlsvkadfpptps 146	
CC	chromosome/segment 3. It was published by Freeman, F.J. et al., J. of Immunology, 143: 8; 2714-2722, 15th October 1989. It can be found in Genbank at Accession No. M27533. The encoded protein, R67989, binds both human CTLA4 and human CD8. It is related to human hb7-2 (see Q81351) and murine hb7 (see Q81372).	CC	QY 121 ISDFEFLPTSNIRRITICSTSGGFPEPHLSWLENGEELNATNTVSODPETLYAVSSKLD 180	
XX	Sequence 288 AA;	XX	Db 147 isdfefiptsnirriticsstsgfpephlswlengeelnaainttvsqdpetelyavsskldf 206	
CC	Q81371 is in pcDM8 vector. It is derived from lymphoid B cells, cell line Raji, clone no. 13. Its position in the genome is	CC	QY 181 NMUTNHSPNCLIKYGHLYRNQTFNWNTTKQEHFPDN 216	
CC	chromosome/segment 3. It was published by Freeman, F.J. et al., J. of Immunology, 143: 8; 2714-2722, 15th October 1989. It can be found in Genbank at Accession No. M27533. The encoded protein, R67989, binds both human CTLA4 and human CD8. It is related to human hb7-2 (see Q81351) and murine hb7 (see Q81372).	CC	Db 207 nmtnhsfmclikyghlyrnqtfnwnttkqehfpdn 242	
CC	Sequence 288 AA;	XX	RESULT 3	
CC	Q81371 is in pcDM8 vector. It is derived from lymphoid B cells, cell line Raji, clone no. 13. Its position in the genome is	CC	AAW67804	
CC	chromosome/segment 3. It was published by Freeman, F.J. et al., J. of Immunology, 143: 8; 2714-2722, 15th October 1989. It can be found in Genbank at Accession No. M27533. The encoded protein, R67989, binds both human CTLA4 and human CD8. It is related to human hb7-2 (see Q81351) and murine hb7 (see Q81372).	CC	ID AAW67804 standard; Protein; 288 AA.	
CC	Sequence 288 AA;	XX	XX	
CC	Q81371 is in pcDM8 vector. It is derived from lymphoid B cells, cell line Raji, clone no. 13. Its position in the genome is	CC	AC AAW67804;	
CC	chromosome/segment 3. It was published by Freeman, F.J. et al., J. of Immunology, 143: 8; 2714-2722, 15th October 1989. It can be found in Genbank at Accession No. M27533. The encoded protein, R67989, binds both human CTLA4 and human CD8. It is related to human hb7-2 (see Q81351) and murine hb7 (see Q81372).	CC	XX	
CC	Sequence 288 AA;	XX	DE Human B7 protein sequence.	
CC	Q81371 is in pcDM8 vector. It is derived from lymphoid B cells, cell line Raji, clone no. 13. Its position in the genome is	CC	XX	
CC	chromosome/segment 3. It was published by Freeman, F.J. et al., J. of Immunology, 143: 8; 2714-2722, 15th October 1989. It can be found in Genbank at Accession No. M27533. The encoded protein, R67989, binds both human CTLA4 and human CD8. It is related to human hb7-2 (see Q81351) and murine hb7 (see Q81372).	CC	KW Human; B7; transfection; mammal; tumour cell; sarcoma; co-stimulation;	
CC	Sequence 288 AA;	XX	XX	
CC	Q81371 is in pcDM8 vector. It is derived from lymphoid B cells, cell line Raji, clone no. 13. Its position in the genome is	CC	AC AAW38414;	
CC	chromosome/segment 3. It was published by Freeman, F.J. et al., J. of Immunology, 143: 8; 2714-2722, 15th October 1989. It can be found in Genbank at Accession No. M27533. The encoded protein, R67989, binds both human CTLA4 and human CD8. It is related to human hb7-2 (see Q81351) and murine hb7 (see Q81372).	CC	XX	
CC	Sequence 288 AA;	XX	XX	
CC	Q81371 is in pcDM8 vector. It is derived from lymphoid B cells, cell line Raji, clone no. 13. Its position in the genome is	CC	DE Human B7 protein sequence.	
CC	chromosome/segment 3. It was published by Freeman, F.J. et al., J. of Immunology, 143: 8; 2714-2722, 15th October 1989. It can be found in Genbank at Accession No. M27533. The encoded protein, R67989, binds both human CTLA4 and human CD8. It is related to human hb7-2 (see Q81351) and murine hb7 (see Q81372).	CC	XX	
CC	Sequence 288 AA;	XX	KW Human; B7; transfection; mammal; tumour cell; sarcoma; co-stimulation;	
CC	Q81371 is in pcDM8 vector. It is derived from lymphoid B cells, cell line Raji, clone no. 13. Its position in the genome is	CC	XX	
CC	chromosome/segment 3. It was published by Freeman, F.J. et al., J. of Immunology, 143: 8; 2714-2722, 15th October 1989. It can be found in Genbank at Accession No. M27533. The encoded protein, R67989, binds both human CTLA4 and human CD8. It is related to human hb7-2 (see Q81351) and murine hb7 (see Q81372).	CC	AC AAW38414;	
CC	Sequence 288 AA;	XX	XX	

Key	Location/Qualifiers	1 GLSHFCSGVIVHTKEYKEVATLSCGHNVSVELAQTRIYQKEKRMVLTMMMSGDMNTIWPE 60
Peptide	1..34 /note= "signal peptide"	Db 27 9lshfcsgvihvtkevatlscghnvsveelaqtivwqekkmvltnmsgdmntiwpe 86
FT Protein	35..288 /note= "mature B7 protein"	Qy 61 YKNRTTIDTDTNNLSIVLALRPSDEGTYECVVLKYEKDAFKREHLLAETVLSVKADPPTPS 120
FT Domain	35..242 /note= "extracellular domain"	Db 87 yknrttidttnnlsivlalrpsdegtycvvlyekdafkrehlavtisvkadfpptps 146
FT Domain	243..269 /note= "transmembrane domain"	Qy 121 ISDFEIPTSNIRRICSTSGGGEPFHISWLENGEELMAINTVQSQPDETELYAVSSKLDF 180
FT Domain	270..288 /note= "intracellular domain"	Db 147 isdfepitsnirricstsgggfpfhiswlengelmaintvqsqdptelyavsskldf 206
Modified-site	53..55 /note= "Asn is N-glycosylated"	Qy 181 NMUTNHSEFMCLIKYGHLRVNQFNFNWNTKQEHFPDN 216
FT Modified-site	89..91 /note= "Asn is N-glycosylated"	Db 207 nmtnhsfmclikyghrvnqfnwnntkqhnfpdn 242
Modified-site	98..100 /note= "Asn is N-glycosylated"	RESULT 4
FT Modified-site	186..188 /note= "Asn is N-glycosylated"	ID AAW73640 standard; Protein; 288 AA.
FT Modified-site	207..209 /note= "Asn is N-glycosylated"	XX
FT Modified-site	211..213 /note= "Asn is N-glycosylated"	AC AAW73640;
FT Modified-site	226..228 /note= "Asn is N-glycosylated"	XX
FT Modified-site	236..234 /note= "Asn is N-glycosylated"	DT 23-MAR-1999 (first entry)
FT Domain	35..139 /note= "Ig V-set domain"	DE Human B7-2 antigen.
FT Domain	140..236 /note= "Ig C-set domain"	XX B7-2 antigen; mammalian tumour cell; T cell costimulation; CD28 ligand;
FT	/note= "Ig C-set domain"	KW CTLA4 ligand; therapy; T-cell response; human.
XX	US58598776-A.	XX Homo sapiens.
PN		OS
XX		XX US5861310-A.
PD	12-JAN-1999.	XX
XX		PD 19-JAN-1999.
PF	03-NOV-1993;	XX
XX	93US-014772.	PF 30-MAY-1995;
PR	03-NOV-1993;	XX 95US-0456104.
XX	93US-014772.	PR 30-MAY-1995;
(DAND ) DANA FARBER CANCER INST INC.		XX 95US-0456104.
(DAND ) HARVARD COLLEGE.		PR 03-NOV-1993;
(PA ) REPLICEN CORP.		XX 93US-014773.
(PA ) REPLICEN CORP.		PA (DAND ) DANA FARBER CANCER INST INC.
PI	Freeman GJ, Glimcher LH, Nadler LM, Ostrand-Rosenberg S;	PI Freeman GJ, Gray GS, Nadler LM;
XX	WPI: 1999-1130394/11.	XX WPI: 1999-1130394/11.
DR	N-PSDB; AAX00757.	DR N-PSDB; AAX00757.
DR	WPI: 1999-119893/10.	XX
DR	N-PSDB; AAX00757.	Tumour cell transfected to express B7-2 molecule - useful for tumour
XX	New modified tumour cells - transfected in order to express a T cell	PT therapy by stimulating T-cell response
PT	costimulatory molecule which allows the induction of an anti-tumour	XX Disclosure; Column 37-40; 27pp; English.
PT	response by T cells	PS Disclosure; Column 31-34; 24pp; English.
XX		XX This sequence is the human B7-2 antigen, which can be used in the
PS		CC method of the invention. The method is for transfecting an isolated
XX		CC mammalian tumour cell with an exogenous nucleic acid molecule encoding a
CC	This sequence represents the amino acid sequence of a human B7 protein.	CC mammalian B7-2 molecule, where the B7-2 molecule is expressed in the
CC	The coding sequence can be used to transfect mammalian tumour (sarcoma)	CC tumour cell so that the B7 protein is expressed by the tumour cell and has the
CC	ability to co-stimulate T cells and bind CD28 or CTLA4 ligand.	CC modified tumour cells can be used for inducing an anti-tumour
CC	The modified tumour cells in a subject and are effective against both	CC T-lymphocyte response in a subject and are effective against both
CC	modified and unmodified tumour cells. The modified tumour cells can	CC modified tumour cells can also be administered to prevent or inhibit metastatic spread of a tumour
CC	also to prevent or inhibit recurrence of a tumour following therapeutic	CC or to prevent or inhibit recurrence of a tumour following therapeutic
CC	treatment.	CC treatment.
XX	Sequence 288 AA;	XX Sequence 288 AA;
Query Match	100 %	Query Match 100.0%; Score 1149; DB 20; Length 288;
Best Local Similarity	100 %	Best Local Similarity 100.0%; Fred. No. 2e-103; Mismatches 0; Indels 0; Gaps 0;
Matches 216;	Conservative 0;	Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 GLSHFCSGVIVHTKEYKEVATLSCGHNVSVELAQTRIYQKEKRMVLTMMMSGDMNTIWPE 60	Qy 1 GLSHFCSGVIVHTKEYKEVATLSCGHNVSVELAQTRIYQKEKRMVLTMMMSGDMNTIWPE 60
Db	27 9lshfcsgvihvtkevatlscghnvsveelaqtivwqekkmvltnmsgdmntiwpe 86	Db 27 9lshfcsgvihvtkevatlscghnvsveelaqtivwqekkmvltnmsgdmntiwpe 86
Qy	61 YKNRTTIDTDTNNLSIVLALRPSDEGTYECVVLKYEKDAFKREHLLAETVLSVKADPPTPS 120	Qy 61 YKNRTTIDTDTNNLSIVLALRPSDEGTYECVVLKYEKDAFKREHLLAETVLSVKADPPTPS 120

Db 87 yknrtfditnnisivialpsdegtyecvkyekdrafrehlaevtkyekadptps 146  
 CC (macrophage). The fusion proteins or peptides are useful for enhancing or  
 CC suppressing T cell-mediated immune responses, e.g. in situations of  
 CC tissue, skin or organ transplantation, or in graft-versus-host disease.  
 CC The proteins are also useful for enhancing the efficacy of vaccination  
 CC against a variety of pathogens, and may also be used to upregulate an  
 CC immune response against a particular pathogen during an infection or  
 CC against a tumour in a tumour-bearing host.  
 XX

Db 121 ISDFEITTSNRRICSTSGGPEPHISWLENGEELNAINTVSDPETYAVSSKLF 180  
 CC

Db 147 isdfelptsnrricstsggpephiswlengeelnaintvsdpetylavsskldf 206  
 CC

Qy 181 NMTTNHSFMCILKYGHLRVNGTENWNTTKQEHFPDN 216  
 CC

Db 207 nmtnhsfmclikyghlrvngtfnwnttkqehfpdn 242  
 CC

RESULT 5  
 RAB37087 100.0%; Score 1149; DB 21; Length 288;  
 ID AAB37087 standard; Protein; 288 AA.  
 XX

AC AAB37087;  
 XX

DT 28-MAR-2001 (first entry)

XX

Human B lymphocyte antigen B7-1.  
 DE X  
 KW Immunomodulator; fusion protein; human; murine; mouse; lymphocyte; CD28;  
 KW antigen; extracellular domain; CTR4; immunoglobulin constant region;  
 KW immunogenicity; tumour; sarcoma; antigen presenting cell; macrophage;  
 KW T cell-mediated immune response; transplantation; vaccination.  
 XX

OS HOMO sapiens.  
 XX

PN US6130316-A.  
 XX

PD 10-OCT-2000.  
 XX

PF 26-JUL-1994; 94US-0280757.  
 XX

PR 26-JUL-1993; 93US-0101624.  
 PR 19-AUG-1993; 93US-0103393.  
 PR 03-NOV-1993; 93US-0147773.  
 XX

PA (DAND ) DANA FARBER CANCER INST INC.  
 PA (REPK ) REPLICIN CORP.  
 XX

PI Freeman GJ, Nadler LM, Gray GS, Greenfield E;  
 XX

WPI; 2000-655681/63.  
 DR N-PDB; AACB4051.  
 DR N-PDB; AACB4051.  
 XX

PT Nucleic acids and fusion proteins of CTLA4/CD28 ligands, useful for  
 PT enhancing or suppressing T cell-mediated immune responses, especially  
 PT during tissue, skin or organ transplantation, or in graft-versus-host  
 PT disease -  
 XX

PS Disclosure; Column 87-90; 83pp; English.  
 XX

CC The invention relates to an isolated nucleic acid molecule encoding a first  
 CC fusion protein comprising a first nucleotide sequence encoding a first  
 CC peptide, and a second nucleotide sequence encoding a second peptide.  
 CC The first nucleotide sequence hybridizes in 6 X sodium chloride/sodium  
 CC citrate (SSC) at 45 deg. C, followed by a wash in 0.2 X SSC at 50 deg. C  
 CC to a portion of a nucleotide sequence which encodes a human or murine  
 CC B lymphocyte antigen (B7-2) extracellular domain. The first peptide has  
 CC the ability to bind CD28 or CTLA4. The first peptide has an amino acid  
 CC sequence that is identical or at least 50% identical with the  
 CC extracellular domain of a human B7-2 Peptide (BAB37085). The second  
 CC peptide is especially an immunoglobulin constant region. This sequence  
 CC represents the human B lymphocyte antigen B7-1. The sequence is used for  
 CC comparison with the B7-2 sequence. The human B7-2 protein is an example  
 CC of a first peptide sequence of the invention. The nucleic acid molecules  
 CC are useful in various expression vectors to direct synthesis of the  
 CC corresponding proteins or peptides in a variety of hosts, particularly  
 CC eukaryotic cells, e.g., mammalian or insect cell culture. The nucleic  
 CC acids are also useful for enhancing the immunogenicity of a mammalian  
 CC cell, e.g., tumour cell (sarcoma) or an antigen presenting cell

Query Match 100.0%; Score 1149; DB 21; Length 288;  
 Best Local Similarity 100.0%; Pred. No. 2e-103;  
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GLSHFPGSVTHVTKEYREVATLSCGHNSVYELAQTRIYKOEKEKRMVLTMMSGDMNTIWIPE 60  
 Db 27 glshfpgsvihvtkeyrevatlschgnvsveelaqtivgkekknvltsmgnwiwe 86  
 Qy 61 YKNRATIDITNNLSIVLAIRPSDEGYTECVLKYEKDAFKREHIAEVTLKSVKADEFPTPS 120  
 Db 87 yknrtiditnnlsivlaairpsdegytecvlkyskafrehlaevtlsvkadptps 146  
 Qy 121 ISDFEITTSNRRICSTSGGPPEPHISWLENGEELNAINTVSDPETYAVSSKLF 180  
 Db 147 isdfelptsnrricstsggpephiswlengeelnaintvsdpetylavsskldf 206  
 Qy 181 NMTTNHSFMCILKYGHLRVNGTENWNTTKQEHFPDN 216  
 Db 207 nmtnhsfmclikyghlrvngtfnwnttkqehfpdn 242  
 RESULT 6  
 AAY99966 6  
 ID AAY99966 standard; Protein; 288 AA.  
 XX  
 AC AAY99966;  
 XX  
 DT 10-JAN-2001 (first entry)  
 DE Human B7 protein.  
 XX  
 B7; human; B cell activation antigen; B lymphocytes;  
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis;  
 KW herpes simplex; influenza; common cold; HIV.  
 XX  
 Homo sapiens.  
 XX  
 Key Peptide 1..34  
 FT FT /label= signal\_peptide  
 FT Domain 35..242  
 FT FT /label= Extracellular\_domain  
 FT Domain 35..138  
 FT FT /label= "Ig V-set domain"  
 FT Modified-site 53..55  
 FT FT /note= "N-linked glycosylation site"  
 FT Modified-site 89..91  
 FT FT /note= "N-linked glycosylation site"  
 FT Modified-site 98..100  
 FT FT /note= "N-linked glycosylation site"  
 FT Domain 139..236  
 FT FT /label= "Ig C-set domain"  
 FT Modified-site 186..188  
 FT FT /note= "N-linked glycosylation site"  
 FT Modified-site 207..209  
 FT FT /note= "N-linked glycosylation site"  
 FT Modified-site 211..213  
 FT FT /note= "N-linked glycosylation site"  
 FT Modified-site 226..228  
 FT FT /note= "N-linked glycosylation site"  
 FT Modified-site 232..234  
 FT FT /note= "N-linked glycosylation site"

PT	Domain	243..269 /label=_Transmembrane_domain	DE	Human B7.1 co-stimulatory molecule.
PT	Domain	270..288 /label=_Intracellular_domain	XX	Human B7.1 co-stimulatory molecule; antigen presenting cell; immune response; cell surface receptor; Major histocompatibility complex; MHC classII; proton motor force; mitochondrial membrane potential; mitochondrial metabolism; cancer; autoimmune disease; glycoprotein; neurodegenerative disorder.
XX	US6071716-A.		KW	
PN			KW	
XX	06-JUN-2000.		KW	
PD			KW	
XX			KW	
PF	15-NOV-1993;	93US-0153262.	OS	Homo sapiens.
XX			XX	W09953953-A2.
PR	28-AUG-1991;	91US-0751306.	PN	
PR	01-OCT-1990;	90US-0591300.	XX	
XX	(DAND ) DANA FARBER CANCER INST INC.		PD	28-OCT-1999.
PA	Nadler LM, Freeman GJ, Freedman AS;		XX	
XX	WPI; 2000-422081/36.		PF	30-MAR-1999;
PI	DR		XX	99WO-US06874.
XX	N-PSDB; AAA6132B.		PR	17-APR-1998; 98US-0082250.
PT	New polynucleotides encoding a B7 activation antigen, useful for regulating T cell mediated immune responses or viral diseases -		PR	29-JUL-1998; 98US-0094519.
XX	PS		PR	24-SEP-1998; 98US-0101580.
XX	PT		XX	(UYVE-) UNIV VERMONT.
XX	PT		PA	PA!
XX	PT		XX	Newell MK;
XX	XX		PT	WPI; 2000-096773/08.
XX	XX		DR	N-PSDB; AAZ29320.
XX	XX		XX	
CC	The present sequence is the unique human B cell activation antigen B7 protein. The cDNA encoding this sequence was isolated from a Burkitt lymphoma cell line cDNA library. Selection of cDNA clones was based on expression of B7, as detected by the anti-B7 monoclonal antibody. The human B7 cDNA was used in hybridisation analysis to isolate the murine B7 cDNA (see AAA6132B). The B7 nucleic acid sequences may be used to generate transgenic, knock-out animals which, in turn, are useful in the development and screening of therapeutically useful reagents. The expressed B7 protein is useful for enhancing or blocking activated T cell mediated immune responses and immune function. Modification of B7 expression is useful in the treatment of autoimmune diseases (e.g. rheumatoid arthritis or multiple sclerosis), herpes simplex, influenza, the common cold and HIV. It is also useful in tissue and organ transplantation.		CC	The present sequence is human B7.1 co-stimulatory molecule. This is a glycoprotein on the surface of antigen presenting cells. This is involved in stimulation of an immune response by its ability to interact with various immune cell surface receptors. The regulation of cell surface expression of MHC classII and co-stimulatory molecule B7 can be manipulated by regulating the intracellular dissipation of proton motor force which can be assessed in terms of mitochondrial membrane potential.
CC			CC	These methods can be used for regulating cell growth and division to control disease processes by manipulating mitochondrial metabolism and the expression of cell surface immune proteins. They can be used for treating diseases associated with excessive cellular division, aberrant differentiation, and premature cellular death, e.g. cancers, autoimmune diseases, neurodegenerative disorders etc.
CC			CC	
CC	Claim 1; Fig 4; 36pp; English.		XX	
CC			XX	
CC	Sequence 288 AA;	0;	CC	
SQ	Query Match 100.0%; Score 1149; DB 21; Length 288; Best Local Similarity 100.0%; Pred. No. 2e-103; Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	0;	CC	
SQ	Query Match 100.0%; Score 1149; DB 21; Length 288; Best Local Similarity 100.0%; Pred. No. 2e-103; Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	0;	CC	
QY	1 GLSHFCSGYVTHVKVEVATLSCGHNSVEELAQTRIYQKEKKMVLTMSGDMNIWPE 60	0;	CC	
Db	27 gishfcsgyvthvekvatlevtscghnsveelaqtriyqkekkmvltmsgdmniwpe 86	0;	CC	
QY	61 YKNRTIFDTINNLISVIALRPSDEGTYECVVLKYEKDAFKREHLAEVTLVQKESKmvltmsgdmniwpe 120	0;	CC	
Db	87 yknrtifdtinnlisvialrpsdegtylecvvlkyekdafkrehlavllsvkadfpips 146	0;	CC	
QY	121 ISDFEIPTSNIRRICSTSGFPPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180	0;	CC	
Db	147 isdfepsnirricstsgfppehlswlengelnaainttvsqdpetelyavsskldf 206	0;	CC	
QY	181 NMTRTNHSFMCOLIKYGHLYRQNTFWNTTKQEHFPDN 216	0;	CC	
Db	207 nmtrtnhsfmcolikyghlyrqtfnwttkqehfpdn 242	0;	CC	
RESULT	7	0;	CC	
AY44289	AY44289 standard; Protein; 288 AA.	0;	CC	
XX		0;	CC	
ID	AY44289	0;	CC	
DT	29-FEB-2000 (first entry)	0;	CC	
XX		0;	CC	
AC	AY44289;	0;	CC	
XX		0;	CC	
RESULT	8	0;	CC	
AY44289	AY44289 standard; Protein; 288 AA.	0;	CC	
XX		0;	CC	
DT	29-FEB-2000 (first entry)	0;	CC	
XX		0;	CC	
RESULT	242	0;	CC	
AY44289	AY44289 standard; Protein; 288 AA.	0;	CC	
XX		0;	CC	
DT	29-FEB-2000 (first entry)	0;	CC	
XX		0;	CC	
RESULT	242	0;	CC	
AY44289	AY44289 standard; Protein; 288 AA.	0;	CC	
XX		0;	CC	
DT	29-FEB-2000 (first entry)	0;	CC	
XX		0;	CC	
RESULT	242	0;	CC	
AY44289	AY44289 standard; Protein; 288 AA.	0;	CC	
XX		0;	CC	
DT	29-FEB-2000 (first entry)	0;	CC	
XX		0;	CC	
RESULT	242	0;	CC	
AY44289	AY44289 standard; Protein; 288 AA.	0;	CC	
XX		0;	CC	
DT	29-FEB-2000 (first entry)	0;	CC	
XX		0;	CC	
RESULT	242	0;	CC	
AY44289	AY44289 standard; Protein; 288 AA.	0;	CC	
XX		0;	CC	
DT	29-FEB-2000 (first entry)	0;	CC	
XX		0;	CC	
RESULT	242	0;	CC	
AY44289	AY44289 standard; Protein; 288 AA.	0;	CC	
XX		0;	CC	
DT	29-FEB-2000 (first entry)	0;	CC	
XX		0;	CC	
RESULT	242	0;	CC	
AY44289	AY44289 standard; Protein; 288 AA.	0;	CC	
XX		0;	CC	
DT	29-FEB-2000 (first entry)	0;	CC	
XX		0;	CC	
RESULT	242	0;	CC	
AY44289	AY44289 standard; Protein; 288 AA.	0;	CC	
XX		0;	CC	
DT	29-FEB-2000 (first entry)	0;	CC	
XX		0;	CC	
RESULT	242	0;	CC	
AY44289	AY44289 standard; Protein; 288 AA.	0;	CC	
XX		0;	CC	
DT	29-FEB-2000 (first entry)	0;	CC	
XX		0;	CC	
RESULT	242	0;	CC	
AY44289	AY44289 standard; Protein; 288 AA.	0;	CC	
XX		0;	CC	
DT	29-FEB-2000 (first entry)	0;	CC	
XX		0;	CC	
RESULT	242	0;	CC	
AY44289	AY44289 standard; Protein; 288 AA.	0;	CC	
XX		0;	CC	
DT	29-FEB-2000 (first entry)	0;	CC	
XX		0;	CC	
RESULT	242	0;	CC	
AY44289	AY44289 standard; Protein; 288 AA.	0;	CC	
XX		0;	CC	
DT	29-FEB-2000 (first entry)	0;	CC	
XX		0;	CC	
RESULT	242	0;	CC	
AY44289	AY44289 standard; Protein; 288 AA.	0;	CC	
XX		0;	CC	
DT	29-FEB-2000 (first entry)	0;	CC	
XX		0;	CC	
RESULT	242	0;	CC	
AY44289	AY44289 standard; Protein; 288 AA.	0;	CC	
XX		0;	CC	
DT	29-FEB-2000 (first entry)	0;	CC	
XX		0;	CC	
RESULT	242	0;	CC	
AY44289	AY44289 standard; Protein; 288 AA.	0;	CC	
XX		0;	CC	
DT	29-FEB-2000 (first entry)	0;	CC	
XX		0;	CC	
RESULT	242	0;	CC	
AY44289	AY44289 standard; Protein; 288 AA.	0;	CC	
XX		0;	CC	
DT	29-FEB-2000 (first entry)	0;	CC	
XX		0;	CC	
RESULT	242	0;	CC	
AY44289	AY44289 standard; Protein; 288 AA.	0;	CC	
XX		0;	CC	
DT	29-FEB-2000 (first entry)	0;	CC	
XX		0;	CC	
RESULT	242	0;	CC	
AY44289	AY44289 standard; Protein; 288 AA.	0;	CC	
XX		0;	CC	
DT	29-FEB-2000 (first entry)	0;	CC	
XX		0;	CC	
RESULT	242	0;	CC	
AY44289	AY44289 standard; Protein; 288 AA.	0;	CC	
XX		0;	CC	
DT	29-FEB-2000 (first entry)	0;	CC	
XX		0;	CC	
RESULT	242	0;	CC	
AY44289	AY44289 standard; Protein; 288 AA.	0;	CC	
XX		0;	CC	
DT	29-FEB-2000 (first entry)	0;	CC	
XX		0;	CC	
RESULT	242	0;	CC	
AY44289	AY44289 standard; Protein; 288 AA.	0;	CC	
XX		0;	CC	
DT	29-FEB-2000 (first entry)	0;	CC	
XX		0;	CC	
RESULT	242	0;	CC	
AY44289	AY44289 standard; Protein; 288 AA.	0;	CC	
XX		0;	CC	
DT	29-FEB-2000 (first entry)	0;	CC	
XX		0;	CC	
RESULT	242	0;	CC	
AY44289	AY44289 standard; Protein; 288 AA.	0;	CC	
XX		0;	CC	
DT	29-FEB-2000 (first entry)	0;	CC	
XX		0;	CC	
RESULT	242	0;	CC	
AY44289	AY44289 standard; Protein; 288 AA.	0;	CC	
XX		0;	CC	
DT	29-FEB-2000 (first entry)	0;	CC	
XX		0;	CC	
RESULT	242	0;	CC	
AY44289	AY44289 standard; Protein; 288 AA.	0;	CC	
XX		0;	CC	
DT	29-FEB-2000 (first entry)	0;	CC	
XX		0;	CC	
RESULT	242	0;	CC	
AY44289	AY44289 standard; Protein; 288 AA.	0;	CC	
XX		0;	CC	
DT	29-FEB-2000 (first entry)	0;	CC	
XX		0;	CC	
RESULT	242	0;	CC	
AY44289	AY44289 standard; Protein; 288 AA.	0;	CC	
XX		0;	CC	
DT	29-FEB-2000 (first entry)	0;	CC	
XX		0;	CC	
RESULT	242	0;	CC	
AY44289	AY44289 standard; Protein; 288 AA.	0;	CC	
XX		0;	CC	
DT	29-FEB-2000 (first entry)	0;	CC	
XX		0;	CC	
RESULT	242	0;	CC	
AY44289	AY44289 standard; Protein; 288 AA.	0;	CC	
XX		0;	CC	
DT	29-FEB-2000 (first entry)	0;	CC	
XX		0;	CC	
RESULT	242	0;	CC	
AY44289	AY44289 standard; Protein; 288 AA.	0;	CC	
XX		0;	CC	
DT	29-FEB-2000 (first entry)	0;	CC	
XX		0;	CC	
RESULT	242	0;	CC	
AY44289	AY44289 standard; Protein; 288 AA.	0;	CC	
XX		0;	CC	
DT	29-FEB-2000 (first entry)	0;	CC	
XX		0;	CC	
RESULT	242	0;	CC	
AY44289	AY44289 standard; Protein; 288 AA.	0;	CC	
XX		0;	CC	
DT	29-FEB-2000 (first entry)	0;	CC	
XX		0;	CC	
RESULT	242	0;	CC	
AY44289	AY44289 standard; Protein; 288 AA.	0;	CC	
XX		0;	CC	
DT	29-FEB-2000 (first entry)	0;	CC	
XX		0;	CC	
RESULT	242	0;	CC	
AY44289	AY44289 standard; Protein; 288 AA.	0;	CC	
XX		0;	CC	
DT	29-FEB-2000 (first entry)	0;	CC	
XX		0;	CC	
RESULT	242	0;	CC	
AY44289	AY44289 standard; Protein; 288 AA.	0;	CC	
XX		0;	CC	
DT	29-FEB-2000 (first entry)	0;	CC	
XX		0;	CC	
RESULT	242	0;	CC	
AY44289	AY44289 standard; Protein; 288 AA.	0;	CC	
XX		0;	CC	
DT	29-FEB-2000 (first entry)	0;	CC	
XX		0;	CC	
RESULT	242	0;	CC	
AY44289	AY44289 standard; Protein; 288 AA.	0;	CC	
XX		0;	CC	
DT	29-FEB-2000 (first entry)	0;	CC	
XX		0;	CC	
RESULT	242	0;	CC	
AY44289	AY44289 standard; Protein; 288 AA.	0;	CC	
XX		0;	CC	
DT	29-FEB-2000 (first entry)	0;	CC	
XX		0;	CC	
RESULT	242	0;	CC	
AY44289	AY44289 standard; Protein; 288 AA.	0;	CC	
XX		0;	CC	
DT	29-FEB-2000 (first entry)	0;	CC	
XX		0;	CC	
RESULT	242	0;	CC	
AY44289	AY44289 standard; Protein; 288 AA.	0;	CC	
XX		0;	CC	
DT	29-FEB-2000 (first entry)	0;	CC	
XX		0;	CC	
RESULT	242	0;	CC	
AY44289	AY44289 standard; Protein; 288 AA.	0;	CC	
XX		0;	CC	
DT	29-FEB-2000 (first entry)	0;	CC	
XX		0;	CC	
RESULT	242	0;	CC	
AY44289	AY44289 standard; Protein; 288 AA.	0;	CC	
XX		0;	CC	
DT	29-FEB-2000 (first entry)	0;	CC	
XX		0;	CC	
RESULT	242	0;	CC	
AY44289	AY44289 standard; Protein; 288 AA.	0;	CC	
XX		0;	CC	
DT	29-FEB-2000 (first entry)	0;	CC	
XX		0;	CC	
RESULT	242	0;</		

ID	AAY54920 standard; Protein; 288 AA.	Qy	121 ISDFEIPTSNIRRIGTSGGFPEPHLSWLENGEELNAINTVSDOPETELYAVSSKLDF 180
XX	AAY54920;	Db	147 isdfeiptsnirrigtsggfpephlswlengeelnaintvsdopetelyavsskldf 206
AC			
XX	14-FEB-2000 (first entry)		
DT			
XX	Human B7.1 protein sequence.	Qy	181 NMTTNHSFMCILKYGHVRNOTEWNNTKQHEFPDN 216
DE		Db	207 nmtnhsfmclkyghvrqntfnwrtkjehtpdn 242
XX			
RW	Interleukin-12; IL-12; fusion protein; tumour; leukaemia; B7.1 protein.	RESULT 9	
XX	IL-12 p40 subunit; gene therapy; tumour; leukaemia; B7.1 protein.	AAU05121	
OS	Homo sapiens.	ID	AAU05121 standard; Protein; 288 AA.
PN	US5994104-A.	XX	
XX		AC	AAU05121;
PD	30-NOV-1999.	XX	
XX	08-NOV-1996; 96US-0751767.	DT	24-OCT-2001 (first entry)
PF		XX	Colorectal tumour antigen CD80.
XX	08-NOV-1996; 96US-0751767.	DE	
PR		XX	Colorectal cancer; immunostimulant; cytostatic; immune response;
XX	(UNLO ) ROYAL FREE HOSPITAL SCHOOL MED.	KW	adenocarcinoma; immunogenic tumour cell; SW620 cell; COLO 205 cell;
PA		KW	SW403 cell; colon; breast; lung; prostate; cancer; vaccine;
XX	Anderson RJ, Prentice HG, MacDonald ID;	XX	tumour antigen CD80.
P1		XX	
XX	DR WPI; 2000-038261/03.	OS	Homo sapiens.
DR	N-PSDB; AAZ40022.	XX	
XX		PN	WO200154716-A2.
PT	Nucleic acid constructs encoding interleukin-12 fusion proteins useful	XX	
PT	for treating leukemia and other cancers -	PD	02-AUG-2001.
XX		XX	
PS	Example; Fig 10; 73pp; English.	PF	26-JAN-2001; 2001WO-US02731.
XX		XX	
CC	This sequence represents the human B7.1 protein sequence.	PR	27-JAN-2000; 2000US-0178498.
CC	The invention relates to an isolated nucleic acid construct (I)	XX	28-FEB-2000; 2000US-0183335.
CC	comprising a region encoding an interleukin-12 (IL-12) fusion protein	PA	(KINM-) KIMMEL CANCER CENT SIDNEY.
CC	(comprising an IL-12 p35 subunit, an IL-12 p40 subunit and a linker	XX	PA (IMMU-) IMMUNE RESPONSE CORP.
CC	peptide (joining the subunits)) and a region encoding a B7 protein. (I)	XX	
CC	may be used to produce IL-12 fusion proteins according to standard	PI	Sobol RE, Shawler DL, Bartholomew RM, Carlo DJ, Gold DP;
CC	recombinant DNA methodologies. The fusion proteins may be produced either	XX	WPI; 2001-502616/55.
CC	in vitro in a fermentation culture or in vivo as part of a gene therapy	DR	N-PSDB; AAS1426.
CC	protocol (in this case (I) is used to transform a patients cells, which	XX	
CC	then secrete the functional polypeptide to supplement the patients own	PT	New composition comprising an allogeneic tumour cell, useful for
CC	production of IL-12 or to rectify mutations which lead to the expression	PT	stimulating an immune response in a patient having an adenocarcinoma,
CC	of inactive polypeptides). The fusion proteins produced in this way may	PT	especially useful for treating colorectal, breast, lung or prostate
CC	be used to treat any disease which responds to IL-12 such as tumours	XX	cancer -
CC	(both solid and dispersed of the kidney, breast, colon, ovarian and	XX	Example 2; Page 130-131; 131pp; English.
CC	cervical tumours and melanomas) and in particular, tumours of the blood	XX	
CC	such as leukemia. Alternatively, the polypeptides may be used as	CC	The invention relates to a composition for stimulating an immune response
CC	antigens in the production of antibodies to IL-12 and to assay for	CC	in a patient having an adenocarcinoma or colorectal cancer. The
CC	CC	composition comprises an allogeneic tumour cell selected from SW620 cell,	
CC	CC	COLO 205 cell and SW403 cell, and a physiological carrier. The allogeneic	
CC	CC	cell stimulates an immune response in an autologous tumour cell in the	
CC	CC	patient. The composition is useful for stimulating an immune response in	
CC	CC	a patient having an adenocarcinoma, e.g. colon, breast, lung or prostate	
CC	CC	adenocarcinoma. The use of allogeneic tumour cells provides a generic	
CC	CC	source of antigen that can be administered to a variety of patients, in	
CC	CC	contrast to using autologous tumour cells, which must be isolated from	
CC	CC	each individual patient. The allogeneic cells are suitable as a cancer	
CC	CC	vaccine and can stimulate an immune response against autologous tumour	
CC	CC	cells of a cancer patient. The present sequence represents the amino acid	
CC	CC	sequence of colorectal tumour antigen CD80 used in the method of the	
CC	CC	invention.	
XX	Sequence 288 AA;	XX	
XX		SQ	
Query Match 100.0%; Score 1149; DB 21; Length 288;			
Best Local Similarity 100.0%; Pred. No. 2e-103; Mismatches 0; Gaps 0;			
Matches 216; Conservative 0; Indels 0; Gaps 0;			
Db 1 GLSHFCGVIVHTKEYKEVATLSCGHNVSEELAQPRIWKEKNVLTMMSGDMNIWIPE 60			
Db 27 gishfcgvivhtkeyvatlscghnvseelaqriwykeknvltnmsgdmniwipe 86			
Qy 61 YKNRTLFIDTINNSIVIALRPSDECITYCVLYKEKDRAFTLAEVTLSVKADEFPTPS 120			
Db 87 yknrtlfidtlnnsivialrpsdecitycvlykekdraftlvkaevtisvadfttps 146			
Query Match 100.0%; Score 1149; DB 22; Length 288;			
Best Local Similarity 100.0%; Pred. No. 2e-103; Mismatches 0; Gaps 0;			
Matches 216; Conservative 0; Indels 0; Gaps 0;			



DE	Human B7.1-murine A5B7 F(ab')2 fusion protein.	KW	B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2;
XX		KW	CD6; T cell activation; inhibition; graft versus host disease;
KW	Anti-CEA antibody; carcinoma antigen; 806.077 Ab; cancer therapy;	KW	transplant rejection; allograft rejection; autoimmune disease;
KW	cancer diagnosis; complementarity determining region.	KW	allergy; therapy; human; hb7.1glu-glu.
XX		XX	
OS	Chimeric - Homo sapiens.	OS	Chimeric - Homo sapiens.
OS	Chimeric - Mus sp.	OS	Chimeric - synthetic.
XX		XX	
PN	WO9742329-A1.	Key	Location/Qualifiers
XX		FT	1..34
PD	13-NOV-1997.	FT	/note= "potential eukaryotic secretory signal"
XX		FT	peptide"
PF	29-APR-1997;	FT	
XX	97WO-GB01165.	Domain	35..242
PR	14-FEB-1997;	FT	/note= "human B7.1 (mature protein) extracellular
XX	97GB-0003103.	FT	domain"
PR	04-MAY-1996;	FT	
XX	96GB-0009405.	Peptide	243..251
PA	(ZENECA LTD.	FT	/note= "Glu-Glu detection/purification tag"
XX		XX	
PI	Copley CG, Edge MD, Emery SC;	PN	WO9858965-A2.
XX		XX	
DR	WPI: 1997-558997/51.	PD	30-DEC-1998.
DR	N-P5DB; AAV17340.	XX	22-JUN-1998; 98WO-EP03791.
XX		PF	
PT	Anti-carcinoembryonic antigen antibody 806.077 Ab - used for	XX	20-JUN-1997; 97EP-0870092.
PT	diagnosis and therapy of cancer	DR	
XX		XX	
PS	Reference Example 3; Page 190-193; 208pp; English.	PA	(INNO-) INNOGENETICS NV.
XX		XX	
CC	This sequence is the human B7.1-murine A5B7 F(ab')2 fusion protein CC (AB7), and is an example of the antibody of the invention. The antibody CC is an anti-CEA (carcinoembryonic antigen) antibody (preferably CC 806.077 Ab). Host cells or transgenic organisms transformed with DNA CC encoding the antibody, are used to make the antibody or conjugate. The CC conjugate is used in a medicament suitable for intravenous CC administration. The conjugate can be used for cancer therapy, selectively CC killing tumour cells. The antibody can be used for in vivo or in vitro CC diagnosis of cancer.	PT	New molecules which bind B7.1 and B7.2 - useful to prevent and treat PT immune diseases including allograft rejection
CC	Sequence 473 AA;	XX	Example 3.1.2; Fig 4; 182PP; English.
XX		XX	This 29 kDa soluble fusion protein, termed hb7.1glu-glu, is composed CC of human co-stimulatory molecule B7.1 extracellular domain fused CC C-terminally to a synthetic Glu-Glu epitope (see AAW90197). It CC was produced from total RNA of Epstein-Barr virus-transformed CC human spleen cells by RT-PCR using primers MR67 and MR45 (see CC AAW1601). The fusion protein has been produced in SF9 Spodoptera CC frugiperda insect cells using a baculovirus expression system. CC The invention relates to molecules such as diabodies, trivalent and CC tetravalent antibodies and small antigen binding peptides which can CC cross-link, or cross-react with, B7.1 and B7.2 expressed on CC professional antigen presenting cells leading to the inhibition of CC antigen-specific T cell activation. Methods to produce such CC molecules are provided. The molecules are used to treat or prevent CC diseases of the immune system, in particular graft rejection, graft CC versus host disease, allergy and autoimmune diseases (claimed).
CC		XX	Sequence 251 AA;
SQ		SQ	Query Match 99.7%; Score 1146; DB 20; Length 251;
			Best Local Similarity 99.5%; pred. No. 3.2e-103;
			Matches 215; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY	1 GLSHFCSGVIAHVKKEVKEYATLSGGHNSVEELAQTRIYQKENKMLTMMMSGDMNIWPE 60	QY	1 GLSHFCSGVIAHVKKEVKEYATLSGGHNSVEELAQTRIYQKENKMLTMMMSGDMNIWPE 60
Db	27 gishfcsgvhvthkevkeyatlsgghnsveelaqtriywqkemv1tmmssgdmniwpe 86	Db	27 gishfcsgvhvthkevkeyatlsgghnsveelaqtriywqkemv1tmmssgdmniwpe 86
QY	61 YKNRTFIDTNISIVILARPSDEGTVCVLYKYEKAFKREHLAEVTLSVKADEFPTPS 120	QY	61 YKNRTFIDTNISIVILARPSDEGTVCVLYKYEKAFKREHLAEVTLSVKADEFPTPS 120
Db	87 yknrtfiddtnisivilarpsdegtvcvlykyekadfkrehlaeaevtlsvkaadfpptps 146	Db	87 yknrtfiddtnisivilarpsdegtvcvlykyekadfkrehlaeaevtlsvkaadfpptps 146
QY	121 ISDPEIPTSNNIRRICSTSGGFPEPHLPSWLENGEELNANTVSDPTELEYAVSSKLF 180	QY	121 ISDPEIPTSNNIRRICSTSGGFPEPHLPSWLENGEELNANTVSDPTELEYAVSSKLF 180
Db	147 isdpeiptsnirricstsggfpephlpswlengelnaaintvsdpetelyavssklf 206	Db	147 isdpeiptsnirricstsggfpephlpswlengelnaaintvsdpetelyavssklf 206
QY	181 NMNTTNHSFPMCLIXYGHLRVNQNTNWNTTKQEHPDN 216	QY	181 NMNTTNHSFPMCLIXYGHLRVNQNTNWNTTKQEHPDN 216
Db	207 nmtnhsfmclikyghlrvnqtnwnttkqehtpdn 242	Db	207 nmtnhsfmclikyghlrvnqtnwnttkqehtpdn 242
RESULT	12		
ID	AAW90208 standard; Protein; 251 AA.		
XX			
AC	AAW90208;		
XX			
DT	10-MAY-1999 (first entry)		
XX			
DE	hb7.1glu-glu soluble fusion protein.		

181 NMNTTNHSFPMCLIKYGHLRVNQNTFNWNNTKQEHPDN 216

182 GLSHFCSGVIAHVKKEVKEYATLSGGHNSVEELAQTRIYQKENKMLTMMMSGDMNIWPE 60

183 YKNRTFIDTNISIVILARPSDEGTVCVLYKYEKAFKREHLAEVTLSVKADEFPTPS 120

184 yknrtfiddtnisivilarpsdegtvcvlykyekadfkrehlaeaevtlsvkaadfpptps 146

185 121 ISDPEIPTSNNIRRICSTSGGFPEPHLPSWLENGEELNANTVSDPTELEYAVSSKLF 180

186 147 isdpeiptsnirricstsggfpephlpswlengelnaaintvsdpetelyavssklf 206

187 207 nmtnhsfmclikyghlrvnqtnwnttkqehtpdn 242



Line, LLC.  
sp.  
o sapiens.  
000136486-A2.  
MAY-2001.  
INOV-2000; 2000WO-GB04317.  
INOV-1999; 99WO-GB03859.  
FEB-2000; 2000GB-00327.  
MAR-2000; 2000GB-005071.

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use of single chain antibody capable of recognizing a disease associated molecule for manufacturing a medicament for preventing and/or treating a disease condition associated with disease associated

卷之三

Claim 3; Fig 2; 118pp; English.

The specification describes the use of a single chain antibody (ScFv), which is capable of recognizing a disease associated molecule in the manufacture of a medicament for the prevention and treatment of a disease condition. The ScFv antibody is useful in the manufacture of a medicament, for affecting a disease *in vivo*, for preparing a pharmaceutical composition, for *in vivo* imaging and/or for adjuvant treatment of a disease. The ScFv antibody is also useful for treating inflammatory diseases including arthritis, hypersensitivity, autoimmune diseases, cancers, central nervous system disorders including Parkinson's disease, periodontal diseases, cardiovascular diseases, gastrointestinal disorders, infections, diabetes, Helicobacter-related diseases, and other immune disorders. The present sequence represents a B7-1.5r1.1 fusion protein which comprises the N-terminus of the 514 ScFv is fused after amino acid 5 of human B7-1.

卷之三

Query Match		Score 99.5%		Score 1143; DB 22;		Length 488;	
Best Local Similarity		100.0%		Pred. No. 1.6e-102;			
Matches 215;		Conservative 0;		Mismatches 0;		Gaps 0;	
Qy	Ds	Qy	Ds	Qy	Ds	Qy	Ds
1	1	G L S H F C S G V I H V T K E Y K E V A T I L S C G H N V S V E B A Q P R I Y W O R E K K M V L T M M S G D M N I W P E	60				
Db	27	g l s h f c s g y i h v t k e y k e v a t i l s c g h n v s v e e a q t r i y w g e k k m v l t m m s g d m n i w p e	86				
Qy	61	Y K N T I F D I T N I N S T I V I A L R P S D E G T E C Y V L K Y E K D A F R E H L A E V T L S Y K A D F P T P S	120				
Db	87	y k n t i f d i t n l s i v i l a l r p s d e g t e c y v l k y e k d a f r e h l a e v t l s y k a d f p t p s	146				
Qy	121	I S D F E I P T S N I R R I C T S G G F P E P H I S W L E N G E E L N A I N T V S Q D P E T E L Y A V S S K L D F	180				
Db	147	i s d f e i p t s n i r r i c t s g f p e p h i s w l e n g e e i n a i n t v s q d p e t e l y a v s s k l d f	206				
Qy	181	N M T N H S F M C L I K Y G H L R Y N O T E W N N T T K O E H F P D	215				
Db	207	n m t n h s f m c l i k y g h l r v n q t f n w n t t k o e h f p d	241				





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OM protein - protein search, using sw model

Run on: April 24, 2002, 15:26:09 ; Search time 12.53 Seconds  
(without alignments)  
387,926 Million cell updates/sec

Title: US-09-454-651b-23  
Perfect score: 1149  
Sequence: 1 GLSHFCGVHVTKEYKEVA.....LRVNQTFNWNTTKQEHFPDN 216

Scoring table: Blosum62  
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

Issued\_Patents\_AA:  
 1: /cgns\_6/podata/2/liaa/5A\_COMB.pep:  
 2: /cgns\_6/podata/2/liaa/5B\_COMB.pep:  
 3: /cgns\_6/podata/2/liaa/6A\_COMB.pep:  
 4: /cgns\_6/podata/2/liaa/6B\_COMB.pep:  
 5: /cgns\_6/podata/2/liaa/PCTUS\_COMB.pep:  
 6: /cgns\_6/podata/2/liaa/backfiles.pep:  
 \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	1149	100.0	288	2	US-09-147-772-2	Sequence 2, Appli
2	1149	100.0	288	2	US-09-147-772-2	Sequence 6, Appli
3	1149	100.0	288	2	US-09-147-772-2	Sequence 23, Appli
4	1149	100.0	288	3	US-09-153-262-2	Sequence 6, Appli
5	1149	100.0	288	3	US-09-153-262-2	Sequence 2, Appli
6	1149	100.0	288	3	US-09-179-744A-29	Sequence 29, Appli
7	1149	100.0	288	4	US-09-180-77B-29	Sequence 29, Appli
8	1149	100.0	288	4	US-09-159-135-2	Sequence 2, Appli
9	1149	100.0	288	4	US-09-205-67A-6	Sequence 6, Appli
10	1149	100.0	288	4	US-09-102-535-19	Sequence 19, Appli
11	1149	100.0	288	5	PCT-US55-02576-19	Sequence 19, Appli
12	1149	100.0	473	4	US-09-171-945-131	Sequence 29, Appli
13	1050	91.4	208	3	US-09-830-172-15	Sequence 15, Appli
14	1050	91.4	208	4	US-09-375-419-15	Sequence 15, Appli
15	48.8	48.8	306	4	US-09-205-69A-17	Sequence 17, Appli
16	561	48.8	306	4	US-09-102-535-17	Sequence 17, Appli
17	561	48.8	306	5	PCT-US55-02576-17	Sequence 17, Appli
18	561	48.8	320	4	US-09-205-69A-2	Sequence 2, Appli
19	561	48.8	320	4	US-09-102-535-2	Sequence 2, Appli
20	561	48.8	320	5	PCT-US55-02576-2	Sequence 2, Appli
21	558	48.6	306	2	US-09-147-772-4	Sequence 8, Appli
22	558	48.6	306	2	US-09-102-535-17	Sequence 17, Appli
23	558	48.6	306	2	US-09-101-624-25	Sequence 25, Appli
24	558	48.6	306	3	US-09-153-262-4	Sequence 4, Appli
25	558	48.6	306	3	US-09-179-744A-31	Sequence 31, Appli
26	558	48.6	306	4	US-09-280-57B-31	Sequence 31, Appli
27	48.6	306	4	US-09-159-135-4	Sequence 4, Appli	

## ALIGNMENTS

RESULT 1  
US-09-147-772-2  
; Sequence 2, Application US/08147772  
; Patent No. 588776  
; GENERAL INFORMATION:  
; APPLICANT: Ostrand-Rosenberg, Suzanne  
; APPLICANT: Bastar, Sivasubramanian  
; APPLICANT: Glincher, Laurie H.  
; APPLICANT: Freeman, Gordon J.  
; APPLICANT: Nadler, Lee M.  
; TITLE OF INVENTION: Tumor Cells With Increased Immunogenicity  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street, Suite 510  
; CITY: Boston  
; STATE: Massachusetts  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/147,772  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mandragouras, Amy E.  
; REGISTRATION NUMBER: 36,207  
; REFERENCE/DOCKET NUMBER: RPI-003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 227-5941  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 288 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; DESCRIPTION: B cell activation antigen; natural ligand  
; DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein  
; DESCRIPTION: for CD28 T cell surface antigen; natural ligand  
; DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein  
; NAME/KEY: signal sequence  
; LOCATION: -34 to -1  
; IDENTIFICATION METHOD: amino terminal sequencing of

IDENTIFICATION METHOD: soluble protein  
 OTHER INFORMATION: hydrophobic  
 FEATURE:  
 NAME/KEY: extracellular domain  
 LOCATION: 1 to 208  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: transmembrane domain  
 LOCATION: 209 to 235  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: intracellular domain  
 LOCATION: 236 to 254  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 19 to 21  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 55 to 57  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 64 to 66  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 152 to 154  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 173 to 175  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 177 to 179  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 192 to 194  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 198 to 200  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: Ig V-set domain  
 LOCATION: 1 to 104  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: Ig C-set domain  
 LOCATION: 105 to 202  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 PUBLICATION INFORMATION:  
 AUTHORS: FREEMAN, GORDON J.  
 AUTHORS: FREEDMAN, ARNOLD S.  
 AUTHORS: SEGLI, JEFFREY M.  
 AUTHORS: LEE, GRACE  
 AUTHORS: WHITMAN, JAMES F.

AUTHORS: NADLER, LEE M.  
 TITLE: B7, A New Member Of The Ig Superfamily With Unique Expression On Activated And Neoplastic B Cells  
 JOURNAL: The Journal of Immunology  
 VOLUME: 143  
 ISSUE: 8  
 PAGES: 2714-2722  
 DATE: 15-OCT-1989  
 RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262  
 US-08-147-772-2  

Query Match	Score 1149;	DB 2;	Length 288;
Best Local Similarity	100.0%;	Pred. No. 4	7e-113;
Matches 216;	Conservative 0;	Mismatches 0;	Indels 0;
QY 1 GLSHFCGGVHYTKVEVATLSCGHNSVVEAQTQYKEKKMVLTMMMSGDMNIWPE 60			
Db 27 GLSHFCGGVHYTKVEVATLSCGHNSVVEAQTQYKEKKMVLTMMMSGDMNIWPE 86			
QY 61 YKNTTIFDITNNLSIVTIALRPSDEGTYECVVKYKEKDFAKREHLAEVTLSVKADFTPTS 120			
Db 87 YKNTTIFDITNNLSIVTIALRPSDEGTYECVVKYKEKDFAKREHLAEVTLSVKADFTPTS 146			
QY 121 ISDFEIPSNIRITCSTSGGFPEPHISWLNGEELNAINTTYSQDPETELYAYSSKLDF 180			
Db 147 ISDFEIPSNIRITCSTSGGFPEPHISWLNGEELNAINTTYSQDPETELYAYSSKLDF 206			
QY 181 NMTTNHSMCLIKYGLRVNQTFNWNTTKQEHFPDN 216			
Db 207 NMTTNHSMCLIKYGLRVNQTFNWNTTKQEHFPDN 242			
RESULT 2			
US-08-456-104-6			
Sequence 6, Application US/08456104			
Patent No. 5861310			
GENERAL INFORMATION:			
APPLICANT: Freeman, Gordon J.			
APPLICANT: Nadler, Lee M.			
APPLICANT: Gray, Gary S.			
TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3 WITH INCREASE			
NUMBER OF SEQUENCES: 8			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: LAHIVE & COCKFIELD			
CITY: Boston			
STATE: Massachusetts			
COUNTRY: USA			
ZIP: 02109			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC DOS/MS-DOS			
SOFTWARE: Patent in Release #1.0., Version #1.25			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/08/456,104			
FILING DATE:			
CLASSIFICATION: 424			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: 08/101,624;			
OPERATING SYSTEM: PC DOS/MS-DOS			
SOFTWARE: Patent in Release #1.0., Version #1.25			
APPLICATION NUMBER: 08/109,393;			
APPLICATION NUMBER: 19-AUG-1993			
ATTORNEY/AGENT INFORMATION:			
NAME: Mandragouras, Amy E.			
REGISTRATION NUMBER: 36,207			
REFERENCE/DOCKET NUMBER: RPI-008			
TELECOMMUNICATION INFORMATION:			
TELEPHONE: (617) 227-7400			
TELEFAX: (617) 227-5941			
INFORMATION FOR SEQ ID NO: 6:			
SEQUENCE CHARACTERISTICS:			



AUTHORS: FREEDMAN, ARNOLD S.  
; AUTHORS: SEGILLI, JEFFREY M.  
; AUTHORS: LEE, GRACE  
; AUTHORS: WHITMAN, JAMES F.  
; AUTHORS: NADLER, LEE M.

TITLE: B7, A New Member Of The Ig Superfamily With Unique Expression On Activated And Neoplastic B Cells  
JOURNAL: The Journal of Immunology  
VOLUME: 143  
ISSUE: 8  
PAGES: 2714-2722  
DATE: 15-OCT-1989  
RELEVANT RESIDUES IN SEQ ID NO: 23: From -26 to 262  
US-08-101-024-23

Query Match 100.0%; Score 1149; DB 2; Length 288;  
Best Local Similarity 100.0%; Pred. No. 4.7e-13;  
Matches 216; Conserv 0; Indels 0; Gaps 0;

QY 1 GLSHFCGIVHVTKEYEATLSCGHNSVSEELAQTRIYQKEKAVMVLTMMSGDMNIWPE 60  
Db 27 GLSHFCGIVHVTKEYEATLSCGHNSVSEELAQTRIYQKEKAVMVLTMMSGDMNIWPE 86

QY 61 YKNRTIFDTINNLSTVTLRPSDETYECVLYKDAFREHLAETVLSVKADEFTPTPS 120  
Db 87 YKNRTIFDTINNLSTVTLRPSDETYECVLYKDAFREHLAETVLSVKADEFTPTPS 146

QY 121 ISDFEPTSNIRRICSTSGGFPEPHLSWLENGEELNAINTVSQDPETELYAVSSKLDF 180  
Db 147 ISDFEPTSNIRRICSTSGGFPEPHLSWLENGEELNAINTVSQDPETELYAVSSKLDF 206

QY 181 NMTTNHSFMCILIKYGLRVNOTFNWNTTKQEHFPDN 216  
Db 207 NMTTNHSFMCILIKYGLRVNOTFNWNTTKQEHFPDN 242

RESULT 5  
US-08-153-262-2  
Sequence 2, Application US/08153262  
; Patent No. 6071716  
; GENERAL INFORMATION:  
; APPLICANT: FREEMAN, GORDON J.  
; APPLICANT: FREEDMAN, ARNOLD S.  
; APPLICANT: NADLER, LEE M.  
; TITLE OF INVENTION: DNA Encoding B7, A New Member Of The IgG Superfamily With Unique Expression On Activated And Neoplastic B Cells.  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: The Dana-  
; STREET: 44 Binney Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02115  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 720kb storage  
; COMPUTER: IBM Personal System 2; Model 30  
; OPERATING SYSTEM: MS/DOS  
; SOFTWARE: Wordperfect 5.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/153\_262  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/751,306  
; FILING DATE: 28-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HARP, JULIE D.  
; REGISTRATION NUMBER: 33132  
; REFERENCE/DOCKET NUMBER: DFCI-116.1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (203) 255-8900  
; FAX: (203) 259-2846  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 288 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; DESCRIPTION:  
; for CD28 T cell surface antigen; natural ligand  
; for CD28 T cell surface antigen; transmembrane protein

RESULT 4  
US-08-751-767A-6  
Sequence 6, Application US/08751767A  
Patent No. 5994104  
GENERAL INFORMATION:  
APPLICANT: ANDERSON, ROBERT J.  
APPLICANT: GRANT, HUGH  
APPLICANT: MACDONALD, IAN D.  
TITLE OF INVENTION: INTERLUKIN-12 FUSION PROTEIN  
NUMBER OF SEQUENCES: 80  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHYE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/751,767A  
FILING DATE: 08-NOV-1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 117-221  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 7038164091  
TELEFAX: 7038164100  
SEQUENCE CHARACTERISTICS:  
LENGTH: ~ 288 amino acids

FEATURE:  
NAME/KEY: signal sequence  
LOCATION: -34 to -1  
IDENTIFICATION METHOD: amino terminal sequencing of  
IDENTIFICATION METHOD: soluble protein  
OTHER INFORMATION: hydrophobic

FEATURE:  
NAME/KEY: extracellular domain  
LOCATION: 1 to 208  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence

FEATURE:  
NAME/KEY: transmembrane domain  
LOCATION: 209 to 235  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence

FEATURE:  
NAME/KEY: intracellular domain  
LOCATION: 236 to 254  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence

FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 19 to 21  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence

FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 55 to 57  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence

FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 64 to 66  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence

FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 152 to 154  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence

FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 173 to 175  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence

FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 177 to 179  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence

FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 192 to 194  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence

FEATURE:  
NAME/KEY: Ig V-set domain  
LOCATION: 1 to 104  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence

FEATURE:  
NAME/KEY: Ig C-set domain  
LOCATION: 105 to 202  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence

AUTHORS: FREEDMAN, ARNOLD S.  
AUTHORS: SEGIL, JEFFREY M.  
AUTHORS: LEE, GRACE F.  
AUTHORS: WHITMAN, JAMES F.  
AUTHORS: NADLER, LEE M.

TITLE: B7, A New Member Of The Ig Superfamily With Unique Expression On Activated And Neoplastic B Cells  
JOURNAL: The Journal of Immunology  
VOLUME: 143  
ISSUE: 8  
PAGES: 2714-2722  
DATE: 15-OCT-1989  
RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262  
US-08-153-262-2

Query Match 100.0%; Score 1149; DB 3; Length 288;  
Best Local Similarity 100.0%; Ped. No. 4 7e-113;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLSHFCGVITHKVEVKATLSCGHNVSVEELAQTIVWQKEKKMVLTMMSGDMNTWPE 60  
Db 27 GLSHFCGVITHKVEVKATLSCGHNVSVEELAQTIVWQKEKKMVLTMMSGDMNTWPE 86

Qy 61 YKRTTIEDTNNSIVILALRPSDEGYECVVLKYEKDAFKREHLAEVTLSYKRADEFPPS 120  
Db 87 YKRTTIEDTNNSIVILALRPSDEGYECVVLKYEKDAFKREHLAEVTLSYKRADEFPPS 146

Qy 121 ISDPEIPTSNRRICTSGGGFPPEPHLSMLENGBELNAINTTVSQDPETELYAVSSKLDF 180  
Db 147 ISDPEIPTSNRRICTSGGGFPPEPHLSMLENGBELNAINTTVSQDPETELYAVSSKLDF 206

Qy 181 NMTTNHSFNMCLIKYGLRVNOTFWNTTKQEHHFDN 216  
Db 207 NMTTNHSFNMCLIKYGLRVNOTFWNTTKQEHHFDN 242

RESULT 6  
US-08-479-744A-29  
Sequence 29, Application US/08479744A  
Patent No. 6084667

GENERAL INFORMATION:  
APPLICANT: Freeman, Gordon J.  
APPLICANT: Nadler, Lee M.  
APPLICANT: Gray, Gary S.

TITLE OF INVENTION: No. 6084667el CTLA4/CD28 Ligands and  
NUMBER OF SEQUENCES: 55

CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/479,744A  
FILING DATE: June 7, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/280,757  
FILING DATE: 26-JUL-1994  
APPLICATION NUMBER: 08/109,393  
FILING DATE: 28-AUG-1993  
APPLICATION NUMBER: 08/101,244  
FILING DATE: 26-JULY-1993  
APPLICATION NUMBER: 08/147,773  
FILING DATE: 3-NOV-1993

ATTORNEY/AGENT INFORMATION:  
 NAME: Mandrajous, Amy E.  
 REGISTRATION NUMBER: 36,207  
 REFERENCE/DOCKET NUMBER: RPI-0044CP3  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 227-7400  
 TELEXFAX: (617) 227-5941  
 INFORMATION FOR SEQ ID NO: 29:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 288 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 DESCRIPTION: B cell activation antigen; natural ligand; transmembrane protein  
 DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein  
 FEATURE:  
 NAME/KEY: signal sequence  
 LOCATION: -34 to -1  
 IDENTIFICATION METHOD: amino terminal sequencing of  
 IDENTIFICATION METHOD: soluble protein  
 OTHER INFORMATION: hydrophobic  
 FEATURE:  
 NAME/KEY: extracellular domain  
 LOCATION: 1 to 208  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: transmembrane domain  
 LOCATION: 209 to 235  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: intracellular domain  
 LOCATION: 236 to 254  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 19 to 21  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 55 to 57  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 64 to 66  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 152 to 154  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 173 to 175  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 177 to 179  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 192 to 194  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation

LOCATION: 198 to 200  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: Ig C-set domain  
 LOCATION: 105 to 202  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 PUBLICATION INFORMATION:  
 AUTHORS: FREEMAN, GORDON J.  
 AUTHORS: FREEDMAN, ARNOLD S.  
 AUTHORS: SEGIL, JEFFREY M.  
 AUTHORS: LEE, GRACE F.  
 AUTHORS: WHITMAN, JAMES F.  
 AUTHORS: NADLER, LEE M.  
 TITLE: B7, A New Member Of The Ig Superfamily With Unique Expression On Activated And Neoplastic B Cells  
 JOURNAL: The Journal of Immunology  
 VOLUME: 143  
 ISSUE: 8  
 PAGES: 2714-2722  
 DATE: 15-OCT-1989  
 RELEVANT RESIDUES IN SEQ ID NO: 29: From -26 to 262  
 US-08-479-744A-29

Query Match Score 1149; DB 3; Length 288;  
 Best Local Similarity 100.0%; Pred. No 4, 7e-113;  
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLSHFCSGVTHVTKVEVATLSCGHNTSYEELAQTRIYQKEKKMVLTTMSGDMNIWPE 60  
 Db 27 GLSHFCSGVTHVTKVEVATLSCGHNTSYEELAQTRIYQKEKKMVLTTMSGDMNIWPE 86

Qy 61 YKNTIDFTINNLISVIALRPSDEGTTECVVLYKEKDAFKREHLAETLSSVKADEFPTPS 120  
 Db 87 YKNTIDFTINNLISVIALRPSDEGTBCVVLKYKEKDAFKREHLAETLSSVKADEFPTPS 146

Qy 121 ISDPEIPTSNIRRICKTSGGFPPEPHLSWLENGEELNAINTVSQDPETELYAVSKLDF 180  
 Db 147 ISDPEIPTSNIRRICKTSGGFPPEPHLSWLENGEELNAINTVSQDPETELYAVSKLDF 206

Qy 181 NMTTNHSFNCMLIKYGHRLRVNQTWNNTQEHFPDN 216  
 Db 207 NMTTNHSFNCMLIKYGHRLRVNQTWNNTQEHFPDN 242

RESULT 7  
 US-08-280-757B-29  
 Sequence 29, Application US/08280757B  
 Patent No. 613016

GENERAL INFORMATION:  
 APPLICANT: Freeman, Gordon J.  
 APPLICANT: Nadler, Lee M.  
 APPLICANT: Gray, Gary S.  
 APPLICANT: Greenfield, Edward  
 TITLE OF INVENTION: No. 6130316el CTLA4/CD28 Ligands and Uses Therefor  
 NUMBER OF SEQUENCES: 53  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LAHIVE & COCKFIELD  
 STREET: 60 State Street, Suite 510  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02109

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/280,757B  
FILING DATE: 26-JUL-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/101,624  
FILING DATE: 26-JULY-1993  
APPLICATION NUMBER: 08/109,393  
FILING DATE: 19-AUG-1993  
APPLICATION NUMBER: 08/147,773  
FILING DATE: 3-NOV-1993

ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: RPI-004CP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 288 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
DESCRIPTION: B cell activation antigen; natural ligand  
for CD28 T cell surface antigen; transmembrane protein

FEATURE:  
NAME/KEY: signal sequence  
LOCATION: -34 to -1  
IDENTIFICATION METHOD: amino terminal sequencing of  
IDENTIFICATION METHOD: soluble protein  
OTHER INFORMATION: hydrophobic

FEATURE:  
NAME/KEY: extracellular domain  
LOCATION: 1 to 208  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence

FEATURE:  
NAME/KEY: transmembrane domain  
LOCATION: 209 to 235  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence

FEATURE:  
NAME/KEY: intracellular domain  
LOCATION: 236 to 254  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence

FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 19 to 21  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence

FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 55 to 57  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence

FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 64 to 66  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence

FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 152 to 154  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence

FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 173 to 175

IDENTIFICATION METHOD: similarity with known  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 177 to 179  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence

FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 192 to 194  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence

FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 198 to 200  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence

FEATURE:  
NAME/KEY: Ig V-set domain  
LOCATION: 1 to 104  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence

FEATURE:  
NAME/KEY: Ig C-set domain  
LOCATION: 105 to 202  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence

PUBLICATION INFORMATION:  
AUTHORS: FREEMAN, GORDON J.  
AUTHORS: FRIEDMAN, ARNOLD S.  
AUTHORS: SEGIL, JEFFREY M.  
AUTHORS: WHITMAN, JAMES F.  
AUTHORS: NADLER, LEE M.  
TITLE: B7, A New Member Of The Ig Superfamily With  
Unique Expression On Activated And Neoplastic B Cells  
JOURNAL: The Journal of Immunology  
VOLUME: 143  
ISSUE: 8  
PAGES: 2714-2722  
DATE: 15-OCT-1989

RELEVANT RESIDUES IN SEQ ID NO: 29: From -26 to 262  
US-08-280-757B-29

Query Match 100.0% Score 1149; DB 4; Length 288;  
Best Local Similarity 100.0%; Fred. No. 4.7e-113;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLSHFSGVIVHTKEYKEVATLSCGGHNVSYELAQTRIYQKEKKMVLTMMSGDMNIWPE 60  
Db 27 GLSHFSGVIVHTKEYKEVATLSCGGHNVSYELAQTRIYQKEKKMVLTMMSGDMNIWPE 86  
Qy 61 YKNRTFDITNNLNLSTVIALRPSDETYECVLYKEDAFKREHLAEVTLSVKADPPTPS 120  
Db 87 YKNRTFDITNNLNLSTVIALRPSDETYECVLYKEDAFKREHLAEVTLSVKADPPTPS 146  
Qy 121 ISDFEPTSNIRRIGTSGGFPPEHLISWLNGEELNAINTVSDQPETELYAVSSKLDF 180  
Db 147 ISDFEPTSNIRRIGTSGGFPPEHLISWLNGEELNAINTVSDQPETELYAVSSKLDF 206  
Qy 181 NMTTNHSFMCLIKYGHLRVNQTFENWNTTKQEHFPDN 216  
Db 207 NMTTNHSFMCLIKYGHLRVNQTFENWNTTKQEHFPDN 242

RESULT 8  
US-09-159-135-2  
Sequence 2, Application US/09159135  
Patent No. 6119905  
GENERAL INFORMATION:  
APPLICANT: Ostrand-Rosenberg, Suzanne  
APPLICANT: Baskar, Sivasubramanian  
APPLICANT: Baskar, Sivasubramanian

APPLICANT: Glimcher, Laurie H.  
 APPLICANT: Freeman, Gordon J.  
 APPLICANT: Nadler, Lee M.  
 TITLE OF INVENTION: Tumor Cells With Increased Immunogenicity  
 NUMBER OF SEQUENCES: 4  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LAITIE & COCKFIELD  
 STREET: 60 State Street, Suite 510  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/159,135  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/147,772  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mandragoras, Any E.  
 REGISTRATION NUMBER: 36,207  
 TELECOMMUNICATION INFORMATION:  
 REFERENCE/DOCKET NUMBER: RP1-003  
 TELEPHONE: (617) 227-7400  
 TELEFAX: (617) 227-5941  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 288 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 DESCRIPTION: B cell activation antigen; natural ligand  
 DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein  
 FEATURE:  
 NAME/KEY: signal sequence  
 LOCATION: -34 to -1  
 IDENTIFICATION METHOD: amino terminal sequencing of  
 IDENTIFICATION METHOD: soluble protein  
 OTHER INFORMATION: hydrophobic  
 FEATURE:  
 NAME/KEY: extracellular domain  
 LOCATION: 1 to 208  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 NAME/KEY: transmembrane domain  
 LOCATION: 209 to 235  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 NAME/KEY: intracellular domain  
 LOCATION: 236 to 254  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 19 to 21  
 IDENTIFICATION METHOD: similarity with known  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 55 to 57  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 64 to 66

IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 152 to 154  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 173 to 175  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 177 to 179  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 192 to 194  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 198 to 200  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: Ig V-set domain  
 LOCATION: 1 to 104  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: Ig C-set domain  
 LOCATION: 105 to 202  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 PUBLICATION INFORMATION:  
 AUTHORS: FREEDMAN, ARNOLD S.  
 AUTHORS: SEGIL, JEFFREY M.  
 AUTHORS: LEE, GRACE  
 AUTHORS: WHITMAN, JAMES F.  
 AUTHORS: NADLER, LEE M.  
 TITLE: B7, A New Member Of the Ig Superfamily With Unique Expression On Activated And Neoplastic B Cells  
 JOURNAL: The Journal of Immunology  
 VOLUME: 143  
 ISSUE: 8  
 PAGES: 2714-2722  
 DATE: 15-OCT-1989  
 RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262  
 US-09-159-135-2

Query Match Score 1149; DB 4; Length 288;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-113; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCSGVTHVKVEVATLSCGHNVSEELAQTRIYQKEKKMVLTMMMSGDMNIVDPE 60  
 Db 27 GLSHFCSGVTHVKVEVATLSCGHNVSEELAQTRIYQKEKKMVLTMMMSGDMNIVDPE 86

QY 61 YKNTTIDTNNSIVIALRPSDEGTVCVLYKFKRELAETVLSVADFPFPPS 120  
 Db 87 YKNTTIDTNNSIVIALRPSDEGTVCVLYKFKRELAETVLSVADFPFPPS 146

QY 121 ISDFEIPSNIRITCSTSGGFPFHLSWLENGEELNAINTVYQDPETELAVSSKLDF 180  
 Db 147 ISFEIPSNIRITCSTSGGFPFHLSWLENGEELNAINTVYQDPETELAVSSKLDF 206

QY 181 NMFTTNHSFMCMLIKYGHFLRNONTNWNTKQEHEFPDN 216

3 RESULT 9 US-08-205-697A-19 ; Sequence 19, Application US/08205697A

; GENERAL INFORMATION: ; APPLICANT: Sharpe, Arlene H. ; ADDRESSEE: LAHIVE & COCKFIELD

; APPLICANT: Borriello, Francescopaolo ; STREET: 28 State Street

; APPLICANT: Freeman, Gordon J. ; CITY: Boston

; APPLICANT: Nadler, Lee M. ; STATE: Massachusetts

; TITLE OF INVENTION: No. 6218510el Forms of T Cell Costimulatory Molecules ; COUNTRY: USA

; NUMBER OF SEQUENCES: 65 ; ZIP: 02109-1875

; TITLE OF INVENTION: and Uses Therefor ; COMPUTER READABLE FORM:

; NUMBER OF SEQUENCES: 61 ; MEDIUM TYPE: Floppy disk

; CORRESPONDENCE ADDRESS: ; COMPUTER: IBM PC Compatible

; ADDRESS: LAHIVE & COCKFIELD ; OPERATING SYSTEM: PC-DOS/MS-DOS

; STREET: 60 State Street, suite 510 ; SOFTWARE: ASCII text

; CITY: Boston ; CURRENT APPLICATION DATA:

; STATE: Massachusetts ; APPLICATION NUMBER: US/08/702,525

; COUNTRY: USA ; FILING DATE:

; ZIP: 02109-1875 ; PRIORITY APPLICATION DATA:

; COMPUTER READABLE FORM: ; APPLICATION NUMBER: US 08/205,697

; MEDIUM TYPE: Floppy disk ; FILING DATE: 02-Mar-1994

; COMPUTER: IBM PC compatible ; ATTORNEY/AGENT INFORMATION:

; OPERATING SYSTEM: PC-DOS/MS-DOS ; NAME: Mandragouras, Amy E.

; SOFTWARE: ASCII text ; REGISTRATION NUMBER: 36,207

; CURRENT APPLICATION DATA: ; REFERENCE/DOCKET NUMBER: BWI-120CPUS

; APPLICATION NUMBER: US/08/205,697A ; TELECOMMUNICATION INFORMATION:

; FILING DATE: 02-Mar-1994 ; TELEPHONE: (617)227-7400

; ATTORNEY/AGENT INFORMATION: ; TELEFAX: (617)227-5941

; NAME: Mandragouras, Amy E. ; INFORMATION FOR SEQ ID NO: 19:

; REGISTRATION NUMBER: 36,207 ; SEQUENCE CHARACTERISTICS:

; REFERENCE/DOCKET NUMBER: BWI-120 ; LENGTH: 288 amino acids

; TELEPHONE: (617)227-7400 ; TYPE: amino acid

; TELEFAX: (617)227-5941 ; TOPOLOGY: linear

; INFORMATION FOR SEQ ID NO: 19 ; MOLECULE TYPE: protein

; SEQUENCE CHARACTERISTICS: ; US-08-205-697A-19

Query Match 100.0%; Score 1149; DB 4; Length 288; ; Best Local Similarity 100.0%; Pred. No. 4.7e-113; ; Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 27 GLSHFCSGVTHVTKEVKEYATLSCGHNVSYELAQTRIYQEKVMVLTMSGDMNWIPE 60 ; YKNRIFTIDITNNLSIVLAIRPSDGETYECVVLKYEKDAFKREHLAEVTLVKADFPPTS 120

Qy 1 GLSHFCSGVTHVTKEVKEYATLSCGHNVSYELAQTRIYQEKVMVLTMSGDMNWIPE 60 ; YKNRIFTIDITNNLSIVLAIRPSDGETYECVVLKYEKDAFKREHLAEVTLVKADFPPTS 146

Db 27 GLSHFCSGVTHVTKEVKEYATLSCGHNVSYELAQTRIYQEKVMVLTMSGDMNWIPE 86 ; YKNRIFTIDITNNLSIVLAIRPSDGETYECVVLKYEKDAFKREHLAEVTLVKADFPPTS 180

Qy 61 YKNRIFTIDITNNLSIVLAIRPSDGETYECVVLKYEKDAFKREHLAEVTLVKADFPPTS 120 ; YKNRIFTIDITNNLSIVLAIRPSDGETYECVVLKYEKDAFKREHLAEVTLVKADFPPTS 206

Db 87 YKNRIFTIDITNNLSIVLAIRPSDGETYECVVLKYEKDAFKREHLAEVTLVKADFPPTS 146 ; ISDFEPIPTSMIRRICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLF 180

Qy 121 ISDFEPIPTSMIRRICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLF 206 ; ISDFEPIPTSMIRRICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLF

Qy 181 NMTTNHSFMLIKYGHLRYNQTFNWNTTKEHFPDN 216 ; Sequence 19, Application US/08205697A-19

Db 207 NMTTNHSFMLIKYGHLRYNQTFNWNTTKEHFPDN 242 ; Sequence 19, Application US/08205697A

Db 147 ISDFEPIPTSMIRRICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLF 206 ; General Information: Novel Forms of T cell Costimulatory Molecules

Qy 181 NMTTNHSFMLIKYGHLRYNQTFNWNTTKEHFPDN 216 ; General Information: Novel Forms of T cell Costimulatory Molecules

Db 207 NMTTNHSFMLIKYGHLRYNQTFNWNTTKEHFPDN 242 ; General Information: Novel Forms of T cell Costimulatory Molecules

RESULT 11 ; Sequence 19, Application PC/TUS9502576

; GENERAL INFORMATION: ; APPLICANT: ; TITLE OF INVENTION: Novel Forms of T cell Costimulatory Molecules

; NUMBER OF SEQUENCES: 65 ; CORRESPONDENCE ADDRESS: ; ADDRESS: LAHIVE & COCKFIELD

; STREET: 60 State Street, suite 510 ; CITY: Boston

STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02109-1875  
 PRIORITY: 02/109-1875  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: ASCII Text  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/02576  
 FILING DATE:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/205,697  
 FILING DATE: 02-Mar-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mandragoras, Amy E.  
 REGISTRATION NUMBER: 36,207  
 REFERENCE/DOCKET NUMBER: BWI-120CPPC  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617)227-7400  
 TELEFAX: (617)227-5941  
 INFORMATION FOR SEQ ID NO: 19:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 288 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 PCT-US95-02576-19

Query Match 100.0%; Score 1149; DB 5; Length 288;  
 Best Local Similarity 100.0%; Pred. No. 4 7e-113;  
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLSHFCGVIVTHKVEVATLSCGHNVSEELAQTRIYQKEKKMVLTMMSGDMNIWPE 60  
 Db 27 GLSHFCGVIVTHKVEVATLSCGHNVSEELAQTRIYQKEKKMVLTMMSGDMNIWPE 86  
 Qy 61 YKNRTIFDITNNLSIVIALRPSDEGTYECVVLYKEVDKFREHLAEVTLVKADFTPS 120  
 Db 87 YKNRTIFDITNNLSIVIALRPSDEGTYECVVLYKEVDKFREHLAEVTLVKADFTPS 146  
 Qy 121 ISDFEIPTSNIRRICSTSQQGGFPEPHLSWLENCEELNAINTYSDQPETELYAVSSKLDF 180  
 Db 147 ISDFEIPTSNIRRICSTSQQGGFPEPHLSWLENCEELNAINTYSDQPETELYAVSSKLDF 206  
 Qy 181 NMTTNHSFMCILKYGLRVNQENWNNTKQEHPDN 216  
 Db 207 NMTTNHSFMCILKYGLRVNQENWNNTKQEHPDN 242

RESULT 13  
 US-08-630-172-15  
 Sequence 15, Application US/08630172  
 ; Sequence 15, Application US/08630172  
 ; Patent No. 606054  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Staerz, Uwe  
 ; TITLE OF INVENTION: NOVEL PRODUCT AND PROCESS FOR T  
 ; TITLE OF INVENTION: LYMPHOCYTE VETO  
 ; NUMBER OF SEQUENCES: 41  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Sheridan Ross & McIntosh  
 ; STREET: 1700 Lincoln Street, 35th Floor  
 ; CITY: Denver  
 ; STATE: Colorado  
 ; COUNTRY: U.S.  
 ; ZIP: 80203  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; FILING DATE:  
 ; CLASSIFICATION: 514  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Connell, Gary J.  
 ; REGISTRATION NUMBER: 32,020  
 ; REFERENCE/DOCKET NUMBER: 2879-36  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (303) 863-9700  
 ; TELEFA: (303) 863-0223  
 ; INFORMATION FOR SEQ ID NO: 15:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 208 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 US-08-630-172-15

Query Match 91.4%; Score 1050; DB 3;  
 Best Local Similarity 95.7%; Pred. No. 7 6e-103;  
 Matches 1; Mismatches 8; Indels 0; Gaps 0;

RESULT 12  
 US-09-171-945-131  
 Sequence 131, Application US/09171945  
 ; Patent No. 6277599  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Edge, Michael Derek  
 ; APPLICANT: Emery, Stephen  
 ; APPLICANT: Copley, Clive Graham  
 ; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said  
 ; FILE REFERENCE: Monoclonal Antibody, and Their Therapeutic Use in an Adept System  
 ; CURRENT APPLICATION NUMBER: US/09/171,945  
 ; CURRENT FILING DATE: 1998-10-29  
 ; PRIOR APPLICATION NUMBER: GB9703103.3  
 ; PRIOR FILING DATE: 1997-02-14  
 ; PRIOR APPLICATION NUMBER: GB9609405.7  
 ; PRIOR FILING DATE: 1996-05-04  
 ; PRIOR APPLICATION NUMBER: PCT/GB97/01165  
 ; PRIOR FILING DATE: 1997-04-29  
 ; NUMBER OF SEQ ID NOS: 131  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 131

Qy 9 VIHTKEVKEVALSCGHNVSVEELAQTRIYWOKEKKMVLTMMSGDMNIWPEYKNRTIFD 68  
 1 Db 1 VIHTKEVKEVALSCGHNVSVEELAQTRIYWOKEKKMVLTMMSGDMNIWPEYKNRTIFD 60

Qy 69 ITNNLSIVITALRPSDEGTYECVVLYKEKDAFKREHLAEVTLSVKADFPPTSIDFEIPT 128  
 Db 61 ITNNKSIVITALRPSDEGTYECVVLYKEKDAFKREHLAEVTLSVKADFPPTSIDFEIPT 120

Qy 129 SNIRRLICSTSGGFPPEPHLSWLENGEELNAINTVSDPTELYAVSSKLDFNMTTNHSF 188  
 Db 121 SNIRRLICSTSGGFPPEPHLSWLENGEELNAINTVSDPTELYAVSSKLDFNMTTNHSF 180

Qy 189 MCLIKYGHLYRNQTFNWNTTKQEHFPDN 216  
 Db 181 MCLIKYGHLYRNQTFNWNTTKQEHFPDN 208

RESULT 15  
 US - 08 - 205 - 697A - 17  
 ; Sequence 17, Application US/08205697A

Qy 144 US-09-375-419-15  
 ; Sequence 15, Application US/09375419

GENERAL INFORMATION:  
 APPLICANT: Steenz, Uwe  
 TITLE OF INVENTION: NOVEL PRODUCT AND PROCESS FOR T  
 TITLE OF INVENTION: LYMPHOCYTE VETO  
 NUMBER OF SEQUENCES: 41  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Sheridan Ross & McIntosh  
 STREET: 1700 Lincoln Street, 35th Floor  
 CITY: Denver  
 STATE: Colorado  
 COUNTRY: U.S.  
 ZIP: 80203  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/375,419  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/630,172  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Connell, Gary J.  
 REGISTRATION NUMBER: 32,020  
 REFERENCE/DOCKET NUMBER: 2879-36  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (303) 863-9700  
 TELEFAX: (303) 863-0223  
 INFORMATION FOR SEQ ID NO: 15:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 208 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

Query Match 91.4%; Score 1050; DB 4; Length 208;  
 Best Local Similarity 95.7%; Pred. No. 7.6e-103;  
 Matches 1; Mismatches 8; Indels 0; Gaps 0;

US-09-375-419-15

Query Match 9 VIHTKEVKEVALSCGHNVSVEELAQTRIYWOKEKKMVLTMMSGDMNIWPEYKNRTIFD 68  
 1 Db 1 VIHTKEVKEVALSCGHNVSVEELAQTRIYWOKEKKMVLTMMSGDMNIWPEYKNRTIFD 60

Qy 69 ITNNLSIVITALRPSDEGTYECVVLYKEKDAFKREHLAEVTLSVKADFPPTSIDFEIPT 128  
 Db 61 ITNNKSIVITALRPSDEGTYECVVLYKEKDAFKREHLAEVTLSVKADFPPTSIDFEIPT 120

Query Match 48.8%; Score 561; DB 4; Length 306;  
 Best Local Similarity 50.7%; Pred. No. 4.3e-51;  
 Matches 41; Mismatches 58; Indels 2; Gaps 2;

Qy 12 VTKEYEVATLSCGHNVSVEELAQTRIYWOKEKKMVLTMMSGDMNIWPEYKNRTIFDITN 71  
 Db 42 LSKSYRKDVLLPCRYNSPHEDESDRYHQHDKTYLVSIAGLKLVWPEYKNRTLYDNT- 100

Qy 72 NLSIVTALRPSDEGTYECVLYKEKDAFKREHLAEVTLSVKADFPPTSIDFEIPTSN1 131  
 Db 101 TYSILIGLVLSDRTYSCVYQKERGTYEVHLALKVLSIKADSPNITESGNPSADT 160

Qy 132 RRICSTSGGFPPEPHLSWLENGEELNAINTVSDPTELYAVSSKLDFNMTTNHSFMCL 191  
 Db 161 KRICFASGGFPKRFWLNGRELPGINTTSQDSELYTISQDLDFTTRNTHIKCL 220

Qy 192 IKYGHLYRNQTFNWNTTKQEHFPDN 216  
 Db 221 IKYGAHVSEDFTEWKPPEDP-PDS 244

Wed Apr 24 15:20:24 2002

us-09-454-651b-23.rai

Page 12

Search completed: April 24, 2002, 15:30:40  
Job time: 271 sec